

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:16:48 ; Search time 43 Seconds
(without alignments)
443.045 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQGS LAPTA.....FLRIRTIASDPDERFFNV 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 100665

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: pirl2:.*
3: pirl3:.*
4: pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	32.8	191	2	VLA-2 protein - pi
2	74	7.2	194	2	beta 8 integrin -
3	71	6.9	164	2	hypothetical prote
4	71	6.9	169	2	hypothetical prote
5	71	6.9	170	2	complement C4 - ch
6	71	6.9	197	2	hypothetical prote
7	70.5	6.9	118	2	hypothetical prote
8	70	6.8	188	2	transcription regu
9	69.5	6.8	148	2	conserved hypotet
10	69	6.7	129	2	hypothetical prote
11	68.5	6.7	148	2	acetyltransferase,
12	68	6.6	171	2	hypothetical prote
13	67.5	6.6	151	2	hypothetical prote
14	67.5	6.6	193	2	Jag-related protei
15	67	6.5	181	2	hypothetical prote
16	67	6.5	197	2	rubrerythrin - Met
17	66.5	6.5	166	2	30S ribosomal prot
18	66.5	6.5	187	2	acetyl transferase
19	66	6.4	138	2	virulence regulato
20	66	6.4	180	2	conserved hypotet
21	65.5	6.4	147	2	Ni,Fe-Hydrogenase
22	65	6.3	86	1	gonadoliberin II p
23	65	6.3	170	2	complement C4 - go
24	65	6.3	189	2	hypothetical prote
25	65	6.3	196	2	acetyltransferase
26	64.5	6.3	190	2	hypothetical prote
27	64	6.2	129	2	hypothetical prote
28	64	6.2	129	2	IS426 transposase
29	64	6.2	129	2	IS 426 transposase

30	64	6.2	131	2	JC7739
31	64	6.2	157	2	T30772
32	63.5	6.2	85	2	A53453
33	63.5	6.2	178	2	AH1330
34	63	6.1	194	2	H89940
35	62.5	6.1	108	2	B75029
36	62.5	6.1	178	2	AH1701
37	62	6.0	161	1	A30477
38	62	6.0	161	1	S04499
39	62	6.0	193	2	T32808
40	61.5	6.0	164	2	D84286
41	61.5	6.0	180	2	D83623
42	61.5	6.0	182	2	B56274
43	61	6.0	102	2	D84397
44	61	6.0	161	1	JT0232
45	61	6.0	161	1	JT0349

ALIGNMENTS

RESULT 1

I47230

VLA-2 protein - pig (fragment)

N:Alternate names: glycoprotein Ia/IIa

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I47230; S21518

R:Bahou, W.F.; Potter, C.L.; Mirza, H.

Blood 84, 3734-3741, 1994

A>Title: The VLA-2 (alpha 2 beta 1) I domain functions as a ligand-specific recognition

A:Reference number: I47230; MUID:95036279; PMID:7949129

A:Accession: I47230

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-191 <BAH>

A:Cross-references: UNIPROT:Q29124; EMBL:Z12137; NID:g2158; PIDN:CAA78125.1; PID:g2159

C:Keywords: Glycoprotein

Query Match 32.8%; Score 336; DB 2; Length 191;
Best Local Similarity 43.9%; Pred. No. 1.9e-23;
Matches 69; Conservative 27; Mismatches 61; Indels 0; Gaps 0;

Qy 42 WSEVQTFRLRLVGLFIDPEQIQVLQVQGESPVHWSLGDFTKKEEVVRAAKNLSREG 101

Db 1 WDAVKNFLKRVQGLDIGPTKTQVGLIQYANRPWFNLNFTKAKEMVEATSHTTQYGG 60

Qy 102 RETKTAQAIWVACTEGFSQSHGRPEAARLLVVVTDGESHDELPALKACEAGRVTRY 161

Db 61 DLITFTKAIQVARDAYSAAAGRGPGATKVMVVVTDGESHDSMLKAVIDOCNNDNIURF 120

Qy 162 GIAVLGHLRRQRPSSFLREIRTIASDPDERFFNV 198

Db 121 GIAVLGVLNRLNALTKNLKEIKAIASIPTEIFYFNV 157

RESULT 2

I51310

beta 8 integrin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C:Accession: I51310

R:Venstrom, K.; Reichardt, L.

Mol. Biol. Cell 6, 419-431, 1995

A>Title: Beta 8 integrins mediate interactions of chick sensory neurons with laminin-1,

A:Reference number: I51310; MUID:95352850; PMID:7542940

A:Accession: I51310

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-194 <VEN>

A:Cross-references: UNIPROT:Q91415; GB:S78729; NID:g1042047; PIDN:AAB34966.1; PID:g10420

C:Superfamily: integrin beta chain; laminin-type EGF-like homology

Db 17 PAG--AAVARRLRGETVHAPAHFV-----EVYGAIRQAVVRQLISDHEGL 60
Qy 65 VGLVOYGESPVHWSLGDFTKKEEVVRAAKNLSRRREGRTKTAQAI---MVACTEGFSQS 121
Db 61 VVVNFLSLPVRWPLKPTQRAIQLRSTHTVA--DGAYVALAEGLGVPLITCDGRLAQS 118
Qy 122 HGRPE 127
Db 119 HGHNAE 124

RESULT 11
G95210
acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95210
R:Tattelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <KUR>
A:Cross-references: UNIPROT:Q97P37; GB:AE005672; PIDN:AAK75880.1; PID:gl4973306; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI807

Query Match 6.7%; Score 68.5; DB 2; Length 148;
Best Local Similarity 25.0%; Pred. No. 50;
Matches 28; Conservative 25; Mismatches 34; Indels 25; Gaps 6;
Qy 9 SFQPGSLAPTAQRCPTMYDVIVLDGNSIYPWSEVQTFRLRL-----VGKLPIDP 60
Db 27 SFQEQW-MGP---RIP-FLTLQLAEGVFSIFDQEFVGFQIKIRLEDSNLHGRFFINP 81
Qy 61 EOIQVGLVOYGESPVHWSLGDFTKE-----EVVRAAKNLSRRREGRE 103
Db 82 QKQEGGL---GSKALRKFSVSLAFENRDIIDSISLVNFEANQRAQNLQKEGFE 130

RESULT 12
H75017
hypothetical protein PAB1243 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75017
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: H75017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <KAW>
A:Cross-references: UNIPROT:Q9UY30; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5058
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1243

Query Match 6.6%; Score 68; DB 2; Length 171;
Best Local Similarity 24.3%; Pred. NO. 65;
Matches 33; Conservative 17; Mismatches 44; Indels 42; Gaps 6;
Qy 40 YPMSEVQTFRLRLVGLKFLIDPEQIQVGLVOYGESP-----VHWSLGDGPF----- 83
Db 52 YS1HSSAMKVLEG-----VGLVQRIKXPGRDRRAYFVATKPNFSEWRSAFYEKI 101

Qy 84 -----RTKEEVVRAAKNLSRRREGRTKTAQAINVACTEGFSQSHGGRPEAAR-LLVVVTD 137
Db 102 LRDIETKESIMRALEEGEQSGSEVEIKEKLMALR-----RNEVARKULTLIMQ 153
Qy 138 GESHGDEELPAALKAC 153
Db 154 FKSE--BELLKVLISC 167

RESULT 13
AF2520
hypothetical protein alr7342 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alr
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2520
R:kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2520
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: UNIPROT:Q8YKP6; GB:BA000020; PIDN:BA877100.1; PID:gl71134541; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7342
A:Gene: plasmid

Query Match 6.6%; Score 67.5; DB 2; Length 151;
Best Local Similarity 26.9%; Pred. No. 63;
Matches 14; Conservative 19; Mismatches 18; Indels 1; Gaps 1;
Qy 50 RRLVGLKFLIDPEQIQVGLVOYGESPVH-EWSLGDFTKEEVVRAAKNLSR 100
Db 95 KRLVAEVEVNRNSVNLTMVQEGQAVVRYLKGTYNTKEQFLQAEANAKQOK 146

RESULT 14
E75544
Jag-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75544
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; J
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <WHI>
A:Cross-references: UNIPROT:Q9RXR1; GB:AE001886; GB:AE000513; NID:g6457921; PIDN:AAF0988
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0246
A:Map position: 1

Query Match 6.6%; Score 67.5; DB 2; Length 193;
Best Local Similarity 24.5%; Pred. No. 84;
Matches 40; Conservative 22; Mismatches 50; Indels 51; Gaps 9;
Qy 13 QGSLAPTAQRCPTMYDVIVLDGNSIYPWSEVQTFRLRLVGLKFLIDPE-QIQVGLVOYG 71
Db 21 ESALPPPA---PDAAPVSAFLHGADE-DPRAVLEQFLAELTAR--IDPGLRVQV----- 68
Qy 72 ESPVHWSLGDFTKEEVVRA---AKNLSRREGRETKTAQAINVACTEGFSQSHGGRPE- 127
Db 69 -----RETEDALEAEISGENAARLAGRDGRTLGAIEVIAVAVLAK-HAGRGDL 115

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:28:38 ; Search time 184 Seconds
(without alignments)
551.042 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQGS LAPTA.....FLREIRTIASDPDERFFNV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 646258

Minimum DB seq length: 0

Maximum DB seq length: 198

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	32.8	191	2 Q29124	sus scrofa
2	299	29.2	156	2 Q1V33	Q1V33 homo sapien
3	103.5	10.1	143	2 Q7J373	Q7J373 bos taurus
4	92	9.0	146	2 O96930	O96930 plasmodium
5	80.5	7.9	153	2 Q8MVN3	Q8MVN3 boltenia vi
6	79.5	7.8	174	2 Q74L73	Q74L73 lactobacill
7	79.5	7.8	179	1 FLA1_PLAAC	FLA1_PLAAC
8	74.5	7.3	181	2 Q8Z2B0	Q8Z2B0 oryza sativ
9	74	7.2	194	2 Q91415	Q91415 gallus gall
10	73	7.1	196	2 Q821E5	Q821E5 streptomyce
11	72.5	7.1	134	2 Q920X7	Q920X7 cavia porce
12	72.5	7.1	184	2 Q63LC8	Q63LC8 burkholderi
13	72.5	7.1	184	2 Q83YN4	Q83YN4 burkholderi
14	72.5	7.1	185	2 Q8KYU9	Q8KYU9 uncultured
15	72.5	7.1	187	2 Q6K2K8	Q6K2K8 oryza sativ
16	72	7.0	156	2 Q894X1	Q894X1 clostridium
17	72	7.0	173	2 Q8Z7U4	Q8Z7U4 oryza sativ
18	72	7.0	197	2 Q8LDZ8	Q8LDZ8 arabidopsis
19	71.5	7.0	108	2 Q8TW93	Q8TW93 methanopyru
20	71.5	7.0	151	2 Q84670	Q84670 myxococcus
21	71	6.9	145	2 Q72BK3	Q72BK3 desulfovibr
22	71	6.9	164	2 Q9RS46	Q9RS46 deinococcus
23	71	6.9	169	2 Q58027	Q58027 pyrococcus
24	71	6.9	170	2 Q28796	Q28796 picrogloss
25	71	6.9	174	2 Q9X957	Q9X957 streptomyce
26	71	6.9	197	2 Q9M0V0	Q9M0V0 arabidopsis
27	70.5	6.9	118	2 Q8Z448	Q8Z448 salmonella
28	70.5	6.9	118	2 Q8ZME3	Q8ZME3 salmonella
29	70.5	6.9	142	2 Q6T825	Q6T825 pectobacter
30	70.5	6.9	166	2 Q7NP32	Q7NP32 gloeobacter
31	70.5	6.9	198	2 Q7RYR1	Q7RYR1 neurospora

32	70	6.8	152	2 Q8MVP6	Q8MVP6 boltenia vi
33	70	6.8	188	2 Q8YHB1	Q8YHB1 bruceella me
34	70	6.8	188	2 Q8GOK2	Q8GOK2 bruceella su
35	69.5	6.8	119	2 Q7XHY1	Q7XHY1 oryza sativ
36	69.5	6.8	148	2 Q8DNN2	Q8DNN2 streptococc
37	69	6.7	129	2 P71978	P71978 mycobacteri
38	69	6.7	129	2 Q7TZO4	Q7TZO4 mycobacteri
39	69	6.7	191	2 Q8ZNE4	Q8ZNE4 streptomyce
40	68.5	6.7	127	2 Q728S1	Q728S1 desulfovibr
41	68.5	6.7	148	2 Q97P37	Q97P37 streptococc
42	68.5	6.7	163	2 Q9HBQ1	Q9HBQ1 homo sapien
43	68.5	6.7	168	2 Q8PZ58	Q8PZ58 methanosarc
44	68	6.6	122	2 Q6Z8A2	Q6Z8A2 oryza sativ
45	68	6.6	133	2 Q98J17	Q98J17 rhizobium l

ALIGNMENTS

RESULT 1

Q29124	ID	Q29124	PRELIMINARY;	PRT;	191 AA.
AC	Q29124;				
DT	01-NOV-1996	(TrEMBLrel. 01, Created)			
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	VLA-2	(Fragment)			
OS	Sus scrofa (Pig)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Endothelial;				
RX	MEDLINE=95036279; PubMed=7949129;				
RA	Bahou W.F., Potter C.L., Mirza H.;				
RT	"The VLA-2 (alpha 2 beta 1) I domain functions as a ligand-specific				
RT	recognition sequence for endothelial cell attachment and spreading:				
RT	molecular and functional characterization."				
RL	Blood 84:3734-3741(1994).				
DR	EMBL; Z12137; CAA78125.1; -.				
DR	PIR; I47230; I47230.				
DR	HSP; P17301; IAOX.				
DR	InterPro; IPR002035; VWF_A.				
DR	Pfam; PF00092; VWA; 1.				
DR	PRINTS; PR00453; VWFADOMAIN.				
DR	SMART; SM00327; VWA; 1.				
DR	PROSITE; PS50234; VWA; 1.				
FT	NON_TER 1				
FT	NON_TER 191				
SQ	SEQUENCE 191 AA; 20896 MW; 2E228B472EC699D8 CRC64;				
Query Match 32.8%; Score 336; DB 2; Length 191;					
Best Local Similarity 43.9%; Pred No. 1e-21; Indels 0; Gaps 0;					
Matches 69; Conservative 27; Mismatches 61;					
Qy	42	WSEVQTELRVLGKLFIDPEIQVGLVQYGSPVHWSLGDFTKEEVVRAAKNLSREG	101		
Db	1	WDAVKNLEKRVQGLDIGPTKQVGLIQYANNPRVFNLTFTKAEVVEATSHTYGG	60		
Qy	102	REYTAQAIWVACTEGFSQSHGRPEARLLVVVTVDGSHDGEELPAALKKACEAGRVTRY	161		
Db	61	DLTNTFKAIQVARDAYSAAAGRPATKVMVVVVDGSHDGLKAVIDQNNNDILRF	120		
Qy	162	GIAVLGHVLRQRDPSSFLREIRTIASDPDERFFNV	198		
Db	121	GIAVLGLNRLNLTAKLKEIKAIASIPTEYFFNV	157		
RESULT 2					
Q71V33	ID	Q71V33	PRELIMINARY;	PRT;	156 AA.
AC	Q71V33;				

```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Integrin alpha 2 (Fragment).
GN Name=ITGA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunicki T.J., Kritzik M.R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035968; AAC94975.1; -.
DR HSSP; P17301; IAOX.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17042 MW; BC7ABD63226C652B CRC64;

Query Match 29.2%; Score 299; DB 2; Length 156;
Best Local Similarity 44.1%; Pred. No. 1.5e-18;
Matches 63; Conservative 24; Mismatches 56; Indels 0; Gaps 0;

Qy 56 LFDPEQIQVGLVQGESPVHWSLGDPRFTKEEVVRAAKNLSRREGRETAKTAAIMVACT 115
Db 3 LDIGPTKQVGLIQYANNPRVFNLTNYKTKKEIMVATQTSQYGGDLTNTFGAIQYARK 62

Qy 116 EGFQSGHGGRPEARLLVVVTDGSHDGEELPALAKACEAGRVTTRYGIAGVLYLRQRD 175
Db 63 YAYSAAGGRSRTAKVMVVVTDGSHDGSMLKAVIDQCNHNDNILRFGIAGVLYLRNALD 122

Qy 176 PSSFLREIRTIASDPDRFFPNV 198
Db 123 TKNLKEIKAIASIPTRYFFNV 145

RESULT 3
QJ7J73 PRELIMINARY; PRT; 143 AA.
AC QJ7J73;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Von Willebrand Factor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Porter C.A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004285; AAB61376.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16099 MW; D472A917993E1C5A CRC64;

Query Match 10.1%; Score 103.5; DB 2; Length 143;
Best Local Similarity 23.6%; Pred. No. 0.29;
Matches 26; Conservative 27; Mismatches 56; Indels 1; Gaps 1;
```

```
Qy 48 FLRLVGLKFLDPEQIQVGLVQGESPVHWSLGDPRFTKEEVVRAAKNLSRREGRETAKT 107
Db 14 FVEVIRRMVDVGQDGIHVTVLQYVYVTVVHSHPREPQSKDVVLQRLREVRVYRGNGTNTG 73

Qy 108 QAIMVACTEGFSQSHGGRPEARLLVVVTDGSHDGEELPALAKACEAGR 156
Db 74 LALQYLSEHSFSASQSDRBPQAPNLVYMTGSPASDKIORMPGDIQLVPIG 123

RESULT 4
O96930 PRELIMINARY; PRT; 146 AA.
AC O96930;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Thrombospondin-related anonymous protein (Fragment).
GN Name=TRAP-2;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Doering C.D., Doering C.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X87840; CAA61109.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 1 1
SQ SEQUENCE 146 AA; 16718 MW; A291357664B9F784 CRC64;

Query Match 9.0%; Score 92; DB 2; Length 146;
Best Local Similarity 23.9%; Pred. No. 3.1;
Matches 32; Conservative 29; Mismatches 49; Indels 24; Gaps 6;

Qy 23 CPTVMVIVVLDGNSIT--YPM-SEVQTFRLRLVGLKFLDPEQIQVGL-----VQ 69
Db 11 CQNYDILTILDESASIGSKNWKSHVIPFTDKIILKDTISKNVHVHGILLFSSKNRDYVT 70

Qy 70 YGSPVHWSLGDPRFTKEEVVRAAKNLSRRE--GRETAKTAAIMVACTEGFSQSHGGRPE 127
Db 71 YGDELRYQ-----KDELLKKVEKLKKDYCGGGTKILGALKYS-LENYTKHKNIRYD 121

Qy 128 AARLLVVVTDGESH 141
Db 122 APKVTILFTDGNEN 135

RESULT 5
Q8MVN3 PRELIMINARY; PRT; 153 AA.
AC Q8MVN3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like protein 3 (Fragment).
GN Name=vwa3;
OS Boltenia villosa.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Boltenia.
OX NCBI_TaxID=63515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22248966; PubMed=12361966;
RA Davidson B.J., Swalla B.J.;
RT "A molecular analysis of ascidian metamorphosis reveals activation of
RL Development 129:4739-4751(2002).
EMBL; AF483028; AAM76108.1; -.
```



```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein O01034_C08.33 (Hypothetical protein
DE P0467G09.7)
GN Name=O01034_C08.33; Synonyms=P0467G09.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005383; BAD01379.1; -.
DR EMBL; AP004694; BAD01303.1; -.
KW Hypothetical protein.
SQ SEQUENCE 181 AA; 20889 MW; 9A2871CF7132993F CRC64;
Query Match 7.3%; Score 74.5; DB 2; Length 181;
Best Local Similarity 25.0%; Pred. No. 1.4e+02;
Matches 38; Conservative 18; Mismatches 41; Indels 55; Gaps 7;
QY 2 ICARVDASFPQGSGLAPTA-----QRCPYMDVVIVLDSNSIYPSEVQTFRLRLVGK 55
DB 6 LCA-----PHGQLSGSHGRRRRRC-----LRELGGG 34
QY 56 LFIDPEQIQVLGVGSPVHWSLGDPRTKKEVVRA-----AKNLSRREG-----ET 104
DB 35 VAVRVQQLAVRVQQL--RAAHVIYVNFSTEEELDRSVDRPQIMDSNLSRRKQARLEH 92
QY 105 KTAQAIMVACTEGFSQSHGGRPEAARLLVVVT 136
DB 93 KTADG-----DERERSSEGRQIAVRLAAVVS 119
RESULT 9
Q91415 PRELIMINARY; PRT; 194 AA.
AC Q91415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Beta 8 integrin (Fragment).
GN Name=beta 8 integrin;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain.
RX MEDLINE=95352850; PubMed=7542940;
RA Venstrom K., Reichardt L.;
RT "Beta 8 integrins mediate interactions of chick sensory neurons with
RT laminin-1, collagen IV, and fibronectin.";
RL Mol. Biol. Cell 6:419-431(1995).
DR EMBL; S78729; AB345966.2; -.
DR PIR; I51310; I51310.
DR HSSP; P05106; IUSG.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR Pfam; PF00362; Integrin_beta.1.
DR PRINTS; PR01186; INTEGRINB.
DR SMART; SM00187; INB; 1.
KW Integrin.
```

```
FT NON_TER 194
SQ SEQUENCE 194 AA; 21847 MW; B845301262330547 CRC64;
Query Match 7.2%; Score 74; DB 2; Length 194;
Best Local Similarity 36.1%; Pred. No. 1.7e+02;
Matches 26; Conservative 7; Mismatches 27; Indels 12; Gaps 3;
QY 75 VHEWSLGD----PRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSH-GGRPEAA 129
DB 67 IHVLSLTDNIAEPRNAVNKQISGNTDTPEGGFDAMLQAAV-----CQSHIGWRKEAK 119
QY 130 RLLVVVTDGESH 141
DB 120 RLLLVMTDQTS 131
RESULT 10
Q82IE5 PRELIMINARY; PRT; 196 AA.
AC Q82IE5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative nitroreductase family protein.
GN OrderedLocustNames=SAV3213;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005034; BAC70924.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
KW Complete proteome.
SQ SEQUENCE 196 AA; 21419 MW; 0860C4DFF936CE39 CRC64;
```

```
Query Match 7.1%; Score 73; DB 2; Length 196;
Best Local Similarity 28.1%; Pred. No. 2.2e+02;
Matches 36; Conservative 15; Mismatches 37; Indels 40; Gaps 6;
QY 58 IDPEIQIV--GLVQYGESPVHWSLGDPRTKKEEVVRAAKNLSR-----REGRETKTAQAI 110
DB 28 VTDEQVQAIYDLVKYGPTAFNQSP-----RLTVRSAAERLVLQHMASGNQPKTATAP 82
QY 111 MVACTEGFSQSHGGRPEAARLLVVVTDGESHDEELPA-----ALKACEAGRVTYGI 163
DB 83 LVA-----ILSADNEPH--EELPALFPHPQAKDVFFAERPARREGA 121
QY 164 AVLGHYLR 171
DB 122 AALNALQ 129
```

RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilailai S., Stevens C., Tumapa S.G., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL NCBI_TaxID=272560; CAH34140.1.
DR ENBL: BX571966; CAH38548.1; -.
SQ SEQUENCE 184 AA; 20280 MW; 4C8ICE777D6078B2 CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 184;
Best Local Similarity 28.1%; Pred. No. 2.2e+02;
Matches 38; Conservative 20; Mismatches 44; Indels 33; Gaps 10;

Qy 53 VGKLFDPGEOIQVLVOYGSPVHEWSLG-----DF---RTKEEVVRAAKNLSRREG--- 101
Db 34 IGAL-MDDPAIDPRLF-----PWLAWHLGVETWKDYWPEQVKRARVKAATRIARKKGTA 87

Qy 102 --RETQTAAIMVACTEGFSQSQGGRRPEAARLLVVVTDSHDGEELPALK-----ACE 154
Db 88 AVREVCASFGANVMREWFEKTPKGRPGTFTMLTV---GARDG--IPATAEYVADIIE 142

Qy 155 AGRVTRYGIAVLGHY 169
Db 143 VDRAKR-GTA--HY 153

RESULT 13
Q63YN4 PRELIMINARY; PRT; 184 AA.

AC Q63YN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative phage protein.
GN ORFNames=BPSI0153;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., K.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.B., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilailai S., Stevens C., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR ENBL: BX571965; CAH34140.1; -.
SQ SEQUENCE 184 AA; 20250 MW; 59C09A777D6078B2 CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 184;
Best Local Similarity 28.1%; Pred. No. 2.2e+02;
Matches 38; Conservative 20; Mismatches 44; Indels 33; Gaps 10;

Qy 53 VGKLFDPGEOIQVLVOYGSPVHEWSLG-----DF---RTKEEVVRAAKNLSRREG--- 101
Db 34 IGAL-MDDPAIDPRLF-----PWLAWHLGVETWKDYWPEQVKRARVKAATRIARKKGTA 87

Qy 102 --RETQTAAIMVACTEGFSQSQGGRRPEAARLLVVVTDSHDGEELPALK-----ACE 154
Db 88 AVREVCASFGANVMREWFEKTPKGRPGTFTMLTV---GARDG--IPATAEYVADIIE 142

Qy 155 AGRVTRYGIAVLGHY 169


```
Db 143 VDRKR-GTA---HY 153
RESULT 14
Q8KYU9
ID Q8KYU9 PRELIMINARY; PRT; 185 AA.
AC Q8KYU9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein HslV.
GN Name=hslv;
OS uncultured proteobacterium.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=153809;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heideberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unexpected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AE008921; AAM48724.1; -.
DR HSSP; P43772; IOFH.
DR MEROPS; T01.006; -.
DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.
DR GO; GO:0004175; F:endoropeptidase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001353; Proteasome_A_B.
DR Pfam; PF00227; Proteasome; 1.
KW Heat shock.
SQ SEQUENCE 185 AA; 19430 MW; 9D882E3B14F28C6C CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 185;
Best Local Similarity 23.1%; Pred. No. 2.2e+02;
Matches 43; Conservative 20; Mismatches 68; Indels 55; Gaps 7;

Qy 13 QGSLAPTA-----QRCPTYMDVIVLDSNSIYPWSEVQTFLLRLVGLKLFIDPEQI 63
Db 30 QVSLGPTVIGKSARKVRLSLPGNDVVVGFAGST-----ADAFLLERLEAKLEATPQOL 84
Qy 64 QVGLVQYGESPVHWSLGDFTKKEVVRAAKNLSRREGRETKTAQAIAIMVACTEGFSQSHG 123
Db 85 QRACVELAK----DW-----RTDKYLQKLEA-----MLIVTDG----- 113
Qy 124 GRPEARLLVVVTGESHGDELPALKAACEAGRVTRYGIAVLGHYLRQRDPSSFLREI 183
Db 114 -----AELLIIITGAGDVLEPSHGIAAI-----GSGGNFALAAARGLQETDLNABEIIARKA 163
Qy 184 RTIASD 189
Db 164 MAIASD 169

RESULT 15
Q6K2K8
ID Q6K2K8 PRELIMINARY; PRT; 187 AA.
AC Q6K2K8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBa0091C16.20 (Hypothetical protein
DE P0519B12.40).
GN Name=OSUNBa0091C16.20; Synonyms=P0519B12.40;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005820; BAD22464.1; -.
DR EMBL; AP004884; BAD21948.1; -.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 20415 MW; 96A0FCC9628681DE CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 187;
Best Local Similarity 26.0%; Pred. No. 2.3e+02;
Matches 53; Conservative 17; Mismatches 73; Indels 61; Gaps 11;

Qy 9 SFQPGSLAPTAORCPTYMDVIVLDSNSI-----YPSSEVQTFLLRLVGLKLFIDPEQI 63
Db 16 SFSPPG-----PLTRDIYILSPNPNIPTPFSYPQSP-----RRLVA----- 52
Qy 64 QVGLVQYGESPVHWSLGDFTKKEVVRAAKNLSRREGRETKTAQAIAIMVACTEGFSQ--- 120
Db 53 -----VAARASGWRLWRLHGWRR-----TGAGGIARR-----TAQVTHDGVGGDARRWR 98
Qy 121 -----SHG-GRPEARLLVVVTGESHGDELPALKAACEAGRVTRYGIAVLG-----H 168
Db 99 HRTTAVVAHGVGRPDYPPSMPVPDGHAGHGRILPD--RPCGHSGT--GTWVSGRAWNR 154
Qy 169 YLRQRDPSSFLREIIRTIASDPDS 192
Db 155 STRAQDPDPLPSLPSMEVAAAVPTD 178

Search completed: April 6, 2005, 14:40:36
Job time : 188 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:15:53 ; Search time 178 Seconds
(without alignments)
430.217 Million cell updates/sec

Title: us-09-647-544-2_COPY_140_337

Perfect score: 1025
Sequence: 1 GICARVDASFQPGSLAPTA.....FLREIRTIASDPDERFFENV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760391 residues

Total number of hits satisfying chosen parameters: 1433677

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	89.0	195	5 AAU76862	Human int
2	912	89.0	195	5 AAU76853	Human int
3	912	89.0	198	8 ADR23227	Human int
4	492	48.0	193	5 AAU76863	Human int
5	492	48.0	193	5 AAU76854	Human int
6	492	48.0	196	8 ADR23228	Human int
7	427	41.7	198	8 ADR23225	Human int
8	424	41.4	192	6 AAE33535	Rat-human
9	424	41.4	192	6 AAE33537	Human alp
10	419	40.9	192	6 AAE33536	Rat alpha
11	417	40.7	195	5 AAU76851	Human int
12	417	40.7	195	5 AAU76860	Human int
13	399	38.9	198	8 ADR23226	Human int
14	393	38.3	198	5 ABP54908	Integrin
15	389	38.0	195	5 AAU76852	Human int
16	389	38.0	195	5 AAU76861	Human int
17	374	36.5	185	4 AAU09125	Human int
18	285.5	27.9	148	4 AAU19634	Human nov
19	285.5	27.9	148	4 AAU19794	Human nov
20	285.5	27.9	148	5 ABP47854	Human pol
21	285.5	27.9	148	5 ABP48014	Human pol
22	285.5	27.9	148	7 ADC10816	Human ext
23	285.5	27.9	148	7 ADC10976	Human pro
24	282	27.5	103	4 AAU19822	Human nov
25	282	27.5	103	4 AAU87675	Novel cen

26	282	27.5	103	5 ABP48042	Human pol
27	282	27.5	103	7 ADC11004	Human pro
28	282	27.5	103	8 ADI54990	Novel hum
29	281	27.4	99	5 ADR41441	Human CD-
30	244	23.8	176	5 ABB78816	Von Wille
31	210.5	20.5	181	4 ABU52684	Cell stru
32	179	17.5	180	5 ABP54907	Von Wille
33	177.5	17.3	195	8 ADR23229	Human int
34	171.5	16.7	192	5 AAU76864	Human int
35	171.5	16.7	192	5 AAU76855	Human int
36	156	15.2	194	8 ADR23223	Human int
37	151	14.7	194	8 ADR23222	Human int
38	149.5	14.6	186	8 ADM97129	Collagen
39	149	14.5	191	5 AAU76859	Human int
40	149	14.5	191	5 AAU76850	Human int
41	148	14.4	180	5 ABB76376	Lymphocyt
42	148	14.4	184	3 AAY82349	Human CD1
43	148	14.4	184	6 ABU07332	Human exp
44	148	14.4	184	8 ADG38995	Human CD1
45	148	14.4	184	8 ADR03370	Human CD1

ALIGNMENTS

RESULT 1

AAU76862
ID AAU76862 standard; protein; 195 AA.

XX AC AAU76862;

XX DT 21-MAY-2002 (first entry)

XX DE Human integrin alpha subunit Alpha 10 variant A domain.

XX KW Human; integrin alpha subunit; A domain; Alpha 10; integrin beta subunit; A-like domain; inflammatory disorder; skeletal muscle injury; restenosis; XW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant; KW antiinflammatory; vasotropic; antiparasitic; vulnery; gene therapy; KW mutcin.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 193 /note= "Wild-type Ile substituted by any other amino acid"

XX FT WO200209737-A1.

XX PN 07-FEB-2002.

XX PD 31-JUL-2001; 2001WO-US023957.

XX PF 31-JUL-2000; 2000US-0221950P.

XX PR 11-JAN-2001; 2001US-00758493.

XX PR 13-MAR-2001; 2001US-00805354.

XX XX (GENO) GEN HOSPITAL CORP.

XX XX Arnaout AM, Li R, Xiong J;

XX XX WPI; 2002-188687/24.

XX PT Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.

XX PS Claim 53; Page; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant

CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, immune complexes, restenosis and parasitic diseases,
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit Alpha 10 variant A domain. Note: This variant
 CC sequence is not featured in the specification but has been derived from
 CC the wild-type protein shown in AAU76853

XX SQ Sequence 195 AA;

Query Match 89.0%; Score 912; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2e-96;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CPTVMDVIVLDGNSNIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 82
 DB 1 CPTVMDVIVLDGNSNIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKAIVMVACTGFSQSHGGRPEAARLLVVVTDGESH 142
 DB 61 FRTKEEVVRAAKNLSRREGRETAKAIVMVACTGFSQSHGGRPEAARLLVVVTDGESH 120
 QY 143 GEELPAALKACEAGRVTRYGIAGVLGHLRQRDPSSFLREIRTIASDPDERFFNV 198
 DB 121 GEELPAALKACEAGRVTRYGIAGVLGHLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 2

AAU76853
 ID AAU76853 standard; protein; 195 AA.

AC AAU76853;

DT 21-MAY-2002 (first entry)

XX Human integrin alpha subunit Alpha 10 A domain.

XX Human; integrin alpha subunit; A domain; Alpha 10; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerability; gene therapy.

XX Homo sapiens.

XX WO200209737-A1.

XX 07-FEB-2002.

XX 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-0221950P.

PR 11-JAN-2001; 2001US-00758493.

PR 13-MAR-2001; 2001US-00805354.

XX (GEO) GEN HOSPITAL CORP.

XX Arnaut AM, Li R, Xiong J;

XX WPI; 2002-188687/24.

XX Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.

XX Example 2; Fig 5; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, immune complexes, restenosis and parasitic diseases,
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit Alpha 10 A domain

XX SQ Sequence 195 AA;

Query Match 89.0%; Score 912; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2e-96;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CPTVMDVIVLDGNSNIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 82
 DB 1 CPTVMDVIVLDGNSNIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKAIVMVACTGFSQSHGGRPEAARLLVVVTDGESH 142
 DB 61 FRTKEEVVRAAKNLSRREGRETAKAIVMVACTGFSQSHGGRPEAARLLVVVTDGESH 120
 QY 143 GEELPAALKACEAGRVTRYGIAGVLGHLRQRDPSSFLREIRTIASDPDERFFNV 198
 DB 121 GEELPAALKACEAGRVTRYGIAGVLGHLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 3

ADR23227
 ID ADR23227 standard; protein; 198 AA.

AC ADR23227;

XX 04-NOV-2004 (first entry)

XX Human integrin alpha 10 subunit A domain.

XX Human; integrin; inflammation; antiinflammatory; vasotropic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..195

XX /label = A_domain

XX Misc-difference 193

XX /note= "Invariant ile residue"

XX WO2004066914-A2.

XX 12-AUG-2004.

XX 12-MAY-2003; 2003WO-US014919.

XX 10-MAY-2002; 2002US-00144259.

XX (GEO) GEN HOSPITAL CORP.

XX Arnaut MA, Li R, Xiong J;

XX WPI; 2004-593980/57.

XX GENBANK; XP_002097.

XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
 PT determining candidate compound for binding to CD11b, and for determining

PT compound as activation-dependent ligand.

PS Disclosure; SEQ ID NO 7; 128pp; English.

XX

CC The present sequence is that of the human integrin alpha 10 subunit A

CC domain. This includes an invariant Ile residue. The invention features

CC variant integrin alpha subunit polypeptides in which the invariant Ile is

CC substituted by Gly, Ala or some other amino acid (e.g. Val) or is

CC deleted. The polypeptide can include part or all of the A domain.

CC Replacing the invariant Ile creates a variant integrin polypeptide that

CC is more active (i.e. in solution has a greater proportion of ligand-

CC forming polypeptides) than the wild-type form of the subunit. Variant

CC integrin polypeptides of the invention are useful in assays for compounds

CC that bind to a variant ligand, that interfere with or enhance the binding

CC of an integrin ligand to integrin, and for identifying activation-

CC specific ligands. They are also useful for generating antibodies, e.g.

CC monoclonal antibodies, which bind to the high efficiency form of an

CC integrin. Some such antibodies recognise an epitope that is either not

CC present or not accessible on an integrin that is in a lower affinity

CC conformation. The invention also provides methods of administering a

CC variant integrin polypeptide, or an antibody that selectively binds it,

CC to identify a ligand which binds to an active integrin. Such assays are

CC useful for diagnosing inflammation, e.g. occult inflammation (e.g.

CC abscess or an active arterioleclerotic lesion). Variant integrin

CC polypeptides can also be used to affect the bioavailability of a variant

CC integrin polypeptide ligand and to treat disorders associated with

CC aberrant or unwanted integrin expression or activity, such as vascular

CC injury.

XX

SQ Sequence 198 AA;

Query Match 89.0%; Score 912; DB 8; Length 198;

Best Local Similarity 100.0%; Pred. No. 2.1e-96;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CPTMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQGESPVHWSLGD 82

Db 1 CPTMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQGESPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETCTAQAIMVACTEGFSQSHGSRPEAARLLVVVTDGESH 142

Db 61 FRTKEEVVRAAKNLSRREGRETCTAQAIMVACTEGFSQSHGSRPEAARLLVVVTDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198

Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 4

AAU76863

ID AAU76863 standard; protein; 193 AA.

AC AAU76863;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human integrin alpha subunit Alpha 11 variant A domain.

XX

KW Human; integrin alpha subunit; A domain; Alpha 11; integrin beta subunit;

KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;

KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;

KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;

mutin.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

PH Key Location/Qualifiers

FT Misc-difference 191

FT /note= "Wild-type Ile substituted by any other amino

FT acid"

XX

PN W0200209737-A1.

XX

XX PD 07-FEB-2002.

XX

XX PF 31-JUL-2001; 2001WO-US023957.

XX

XX PR 31-JUL-2000; 2000US-0221950P.

XX

XX PR 11-JAN-2001; 2001US-00758493.

XX

XX PR 13-MAR-2001; 2001US-00805354.

XX

XX PA (GEO) GEN HOSPITAL CORP.

XX

XX PI Arnaout AM, Li R, Xiong J;

XX

XX DR WPI; 2002-188687/24.

XX

XX Novel high affinity integrin polypeptide useful for treating restenosis

PT and parasitic diseases, comprises all or part of variant integrin alpha

PT subunit A domain or variant integrin beta subunit A-like domain.

XX

XX Claim 57; Page; 55pp; English.

XX

CC The invention relates to a high affinity integrin polypeptide comprising

CC all or part of a variant integrin alpha subunit A domain or a variant

CC integrin beta subunit A-like domain. The polypeptide, preferably the

CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by

CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or

CC V at residue 315 and A at residue 320 have been replaced by C, is useful

CC for determining if a test compound is a candidate compound for binding to

CC CD11b or for treating an inflammatory disorder, by contacting a test

CC compound with the polypeptide and determining if the test compound binds

CC to the polypeptide. The integrin subunits are useful for reducing

CC skeletal muscle injury, for treating disorders caused by ischaemia-

CC reperfusion injury, immune complexes, restenosis and parasitic diseases,

CC to purify variant integrin polypeptide ligands and as bait proteins in

CC two-hybrid or three-hybrid assays. This sequence represents a human

CC integrin alpha subunit Alpha 11 variant A domain. Note: This variant

CC sequence is not featured in the specification but has been derived from

CC the wild-type protein shown in AAU76854

XX

SQ Sequence 193 AA;

Query Match 48.0%; Score 492; DB 5; Length 193;

Best Local Similarity 54.5%; Pred. No. 6.4e-48;

Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQGESPVHWSLGD 82

Db 1 CPTMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQGESPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETCTAQAIMVACTEGFSQSHGSRPEAARLLVVVTDGESH 142

Db 61 YRSVKDVVEAASHTEQRGGTETRTAFGIEFARSAFQK--GGRGAKKVMIVITDGESH 118

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198

Db 119 SPDLEKVIQOSERNVTRYAVAVLGYNRRNGINPFTFLNEIKYIASDPDKHFFNV 174

RESULT 5

AAU76854

ID AAU76854 standard; protein; 193 AA.

XX

AC AAU76854;

XX

XX

DT 21-MAY-2002 (first entry)

XX

DE Human integrin alpha subunit Alpha 11 A domain.

XX

KW Human; integrin alpha subunit; A domain; Alpha 11; integrin beta subunit;

KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;

KW ischaemia-reperfusion injury; immune complex; parasitic disease;

KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.

XX

```
OS Homo sapiens.
XX WO200209737-A1.
XX 07-FEB-2002.
XX 31-JUL-2001; 2001WO-US023957.
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX (GEO) GEN HOSPITAL CORP.
XX Arnaout AM, Li R, Xiong J;
XX WPI; 2002-198687/24.
XX Novel high affinity integrin polypeptide useful for treating restenosis
XX and parasitic diseases, comprises all or part of variant integrin alpha
XX subunit A domain or variant integrin beta subunit A-like domain.
XX Example 2; Fig 5; 55pp; English.
XX The invention relates to a high affinity integrin polypeptide comprising
XX all or part of a variant integrin alpha subunit A domain or a variant
XX integrin beta subunit A-like domain. The polypeptide, preferably the
XX CD11b alpha subunit A domain, where I at residue 332 has been replaced by
XX G or A, F at residue 313 and A at residue 320 have been replaced by C, or
XX V at residue 315 and A at residue 320 have been replaced by C, is useful
XX for determining if a test compound is a candidate compound for binding to
XX CD11b or for treating an inflammatory disorder, by contacting a test
XX compound with the polypeptide and determining if the test compound binds
XX to the polypeptide. The integrin subunits are useful for reducing
XX skeletal muscle injury, for treating disorders caused by ischaemia-
XX reperfusion injury, immune complexes, restenosis and parasitic diseases,
XX to purify variant integrin polypeptide ligands and as bait proteins in
XX two-hybrid or three-hybrid assays. This sequence represents the human
XX integrin alpha subunit Alpha 11 A domain
XX Sequence 193 AA;
Query Match 48.0%; Score 492; DB 5; Length 193;
Best Local Similarity 54.5%; Pred. No. 6.4e-48;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;
QY 23 CPTYMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPDQIQVLVQYGSPPHWSLGD 82
DB 1 CQTYMDIVIVLDGNSIYPWVEVQHFLNLTKKFIYIGPGQIQGVVQYGEDVWVHEFLND 60
QY 83 FRTKEEVVRAAKNLSRRREGRETAKQAIMVACTGFQSQSHGGRPEARLLVWVTDGSHD 142
DB 61 YRSVKDVVEAASHIEQGGTETRTAFGIEPARSEAFQK--GGRGAKKVMIVITDGSHD 118
QY 143 GEELPAALKAACEAGRVTRYGIVGLHYLRQRDPSSFLREIRTIASDPDRFFPNV 198
DB 119 SPDLKVIQOSERDNTVRYAVAVLGYNNRRGINPETFLEIKVIASDPDDKHFNV 174
RESULT 6
ID ADR23228 standard; protein; 196 AA.
XX ADR23228;
XX ADR23228;
XX 04-NOV-2004 (first entry)
XX Human integrin alpha 11 subunit A domain.
XX Human; integrin; inflammation; antiinflammatory; vasototropic.
XX Homo sapiens.
XX
```

```
PH Key Location/Qualifiers
FT Domain 1..193
FT Misc-difference 191 /label = A_domain
FT /note= "Invariant Ile residue"
XX WO2004066914-A2.
XX 12-AUG-2004.
XX 12-MAY-2003; 2003WO-US014919.
XX 10-MAY-2002; 2002US-00144259.
XX (GEO) GEN HOSPITAL CORP.
XX Arnaout MA, Li R, Xiong J;
XX WPI; 2004-593980/57.
XX GENBANK; NP_036343.
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
XX determining candidate compound for binding to CD11b, and for determining
XX compound as activation-dependent ligand.
XX Disclosure; SEQ ID NO 8; 128pp; English.
XX The present sequence is that of the human integrin alpha 11 subunit A
XX domain. This includes an invariant Ile residue. The invention features a
XX variant integrin alpha subunit polypeptides in which the invariant Ile is
XX substituted by Gly, Ala or some other amino acid (e.g. Val) or is
XX deleted. The polypeptide can include part or all of the A domain.
XX Replacing the invariant Ile creates a variant integrin polypeptide that
XX is more active (i.e. in solution has a greater proportion of ligand-
XX forming polypeptides) than the wild-type form of the subunit. Variant
XX integrin polypeptides of the invention are useful in assays for compounds
XX that bind to a variant ligand, that interfere with or enhance the binding
XX of an integrin ligand to integrin, and for identifying activation-
XX specific ligands. They are also useful for generating antibodies, e.g.
XX monoclonal antibodies, which bind to the high efficiency form of an
XX integrin. Some such antibodies recognise an epitope that is either not
XX present or not accessible on an integrin that is in a lower affinity
XX conformation. The invention also provides methods of administering a
XX variant integrin polypeptide, or an antibody that selectively binds it,
XX to identify a ligand which binds to an active integrin. Such assays are
XX useful for diagnosing inflammation, e.g. occult inflammation (e.g.
XX abscess or an active arteriosclerotic lesion). Variant integrin
XX polypeptides can also be used to affect the bioavailability of a variant
XX integrin polypeptide ligand and to treat disorders associated with
XX aberrant or unwanted integrin expression or activity, such as vascular
XX injury.
XX Sequence 196 AA;
Query Match 48.0%; Score 492; DB 8; Length 196;
Best Local Similarity 54.5%; Pred. No. 6.5e-48;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;
QY 23 CPTYMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPDQIQVLVQYGSPPHWSLGD 82
DB 1 CQTYMDIVIVLDGNSIYPWVEVQHFLNLTKKFIYIGPGQIQGVVQYGEDVWVHEFLND 60
QY 83 FRTKEEVVRAAKNLSRRREGRETAKQAIMVACTGFQSQSHGGRPEARLLVWVTDGSHD 142
DB 61 YRSVKDVVEAASHIEQGGTETRTAFGIEPARSEAFQK--GGRGAKKVMIVITDGSHD 118
QY 143 GEELPAALKAACEAGRVTRYGIVGLHYLRQRDPSSFLREIRTIASDPDRFFPNV 198
DB 119 SPDLKVIQOSERDNTVRYAVAVLGYNNRRGINPETFLEIKVIASDPDDKHFNV 174
RESULT 7
ADR23225
```


CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC rat-human alpha 1-I domain fusion protein, RdeltaH. This sequence is used
 CC in the exemplification of the invention. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX Sequence 192 AA;
 SQ

Query Match 41.4%; Score 424; DB 6; Length 192;
 Best Local Similarity 47.1%; Pred. No. 4.5e-40;
 Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFRLRLVGLKFLFDPEQIQVGLVQYQGESPVHWSLGDPR 84
 Db 1 TQLDIVIVLDGNSIYPWSEVQTFRLRLVGLKFLFDPEQIQVGLVQYQGESPVHWSLGDPR 60

Qy 85 TKEEVVPAKNLSRREGRETQAQIMVACTEGFSQSHGGRPEARLLVVVTGDSHGE 144
 Db 61 STEEVLVAANKIVQGRGTMTALGDTARKEAFTEARGARRGVKKVMVIVTGESHDNY 120

Qy 145 ELPAALKACAGRVTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFNV 198
 Db 121 RLKXVIQDCEDNIQRFSAIILGHNNGNSTEKFVEEIKSIASEPTEKHFNV 174

RESULT 9
 AAEE33537
 ID AAEE33537 standard; protein; 192 AA.
 AC AAEE33537;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human alpha 1-I domain protein #1.
 XX
 KW Human; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; alpha 1-I protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200283854-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US011521.
 XX
 PR 13-APR-2001; 2001US-0283794P.
 PR 06-JUN-2001; 2001US-0303699P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX
 XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 PT
 XX WPI; 2003-093009/08.
 XX
 PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-

PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.
 XX
 PS Example 24; Page 94; 248pp; English.
 XX
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; betal containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human 1-I domain protein. This sequence is used in the exemplification of
 CC the invention
 XX
 SQ Sequence 192 AA;
 Query Match 41.4%; Score 424; DB 6; Length 192;
 Best Local Similarity 47.1%; Pred. No. 4.5e-40;
 Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFRLRLVGLKFLFDPEQIQVGLVQYQGESPVHWSLGDPR 84
 Db 1 TQLDIVIVLDGNSIYPWSEVQTFRLRLVGLKFLFDPEQIQVGLVQYQGESPVHWSLGDPR 60

Qy 85 TKEEVVPAKNLSRREGRETQAQIMVACTEGFSQSHGGRPEARLLVVVTGDSHGE 144
 Db 61 STEEVLVAANKIVQGRGTMTALGDTARKEAFTEARGARRGVKKVMVIVTGESHDNY 120

Qy 145 ELPAALKACAGRVTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFNV 198
 Db 121 RLKXVIQDCEDNIQRFSAIILGHNNGNSTEKFVEEIKSIASEPTEKHFNV 174

RESULT 10
 AAEE33536
 ID AAEE33536 standard; protein; 192 AA.
 XX
 AC AAEE33536;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Rat alpha 1-I domain protein #1.
 XX
 KW Rat; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; alpha 1-I protein.
 XX
 OS Rattus sp.

XX WO200283854-A2.
 XX 24-OCT-2002.
 XX 12-APR-2002; 2002WO-US011521.
 XX 13-APR-2001; 2001US-0283794P.
 PR 06-JUL-2001; 2001US-0303689P.
 XX (BIOJ) BIOGEN INC.
 XX Lyne PD, Garber EA, Saldanha JW, Karpueas M;
 XX WPI; 2003-093009/08.
 XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.
 XX Example 24; Page 93-94; 248pp; English.
 XX The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; beta1 containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC parietaritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, rheumatoid arthritis, multiple
 CC sclerosis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC rat 1-1 domain protein. This sequence is used in the exemplification of
 CC the invention
 XX the invention
 SQ Sequence 192 AA;
 Query Match 40.9%; Score 419; DB 6; Length 192;
 Best Local Similarity 46.6%; Pred. No. 1.7e-39;
 Matches 81; Conservative 33; Mismatches 60; Indels 0; Gaps 0;
 QY 25 TYMDVIVLDGNSIYPWSEVOTFLRLVGLKFLDPQIQVGLVQYGESPVHWSLGD 84
 Db 1 TQLDIVIVLDGNSIYPWSEVIAFLNDLLKMDLGPQTQVIGVQYGENVTHEFNLYS 60
 QY 85 TKEEVVRAAKNLSRREGRETAKQAQIMVACTEGFSQSHGGRPEAARLLVVVTDGSHD 144
 Db 61 STEEVLVAANKIGRQGLQTMALGIDTARKEAFTARGARGVKKVMVIVTDGSHDNY 120
 QY 145 ELPAALKACEAGRVTRYGVIAVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 Db 121 RLKQVQDCEDENQRFSAIILGHNRLSTEFKFEVEIKSIASEPTKHFNV 174
 RESULT 11
 AAU76851
 ID AAU76851 standard; protein; 195 AA.
 XX AC AAU76851;
 XX DT 21-MAY-2002 (first entry)
 XX

DE Human integrin alpha subunit Alpha 1 (CD49a) A domain.
 XX Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 1;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
 XX Homo sapiens.
 OS WO200209737-A1.
 XX 07-FEB-2002.
 PD 31-JUL-2001; 2001WO-US023957.
 XX 31-JUL-2000; 2000US-0221950P.
 PR 11-JAN-2001; 2001US-00758493.
 PR 13-MAR-2001; 2001US-00805354.
 XX (GEHO) GEN HOSPITAL CORP.
 PA Arnaout AM, Li R, Xiong J;
 PI WPI; 2002-188687/24.
 DR Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX Example 2; Fig 5; 55pp; English.
 XX The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit Alpha 1 (CD49a) A domain
 XX Sequence 195 AA;
 SQ Query Match 40.7%; Score 417; DB 5; Length 195;
 Best Local Similarity 45.5%; Pred. No. 3e-39;
 Matches 80; Conservative 34; Mismatches 62; Indels 0; Gaps 0;
 QY 23 CPTVMDVIVLDGNSIYPWSEVOTFLRLVGLKFLDPQIQVGLVQYGESPVHWSLGD 82
 Db 1 CSTQLDIVIVLDGNSIYPWDSVTAFLNDLLKMDIGKQIQVIGVQYGENVTHEFNLYS 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKQAQIMVACTEGFSQSHGGRPEAARLLVVVTDGSHD 142
 Db 61 YSSTEVLVAANKIVQGRGQTMTALGTDRTARKEAFTARGARGVKKVMVIVTDGSHD 120
 QY 143 GEELPAALKACEAGRVTRYGVIAVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 Db 121 NHRLKKVQDCEDENLQRFSAIILGHNRLSTEFKFEVEIKSIASEPTKHFNV 176
 RESULT 12
 AAU76860
 ID AAU76860 standard; protein; 195 AA.
 XX AC AAU76860;
 XX DT 21-MAY-2002 (first entry)
 XX

XX DE Human integrin alpha subunit Alpha 1 (CD49a) variant A domain.
XX XX
XX Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antiinflammatory; vasotropic; antiparasitic; vulnery; gene therapy;
KW mutin; Alpha 1.
XX XX
XX Homo sapiens.
OS Synthetic.
XX XX
XX Key Location/Qualifiers
FH Misc-difference 193 /note= "Wild-type Ile substituted by any other amino
FT acid"
FT
XX WO200209737-A1.
XX
XX 07-FEB-2002.
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
PI WPI; 2002-188687/24.
XX
XX Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
XX Claim 45; Page; 55pp; English.
XX
XX The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
CC V at residue 315 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents a human
CC integrin alpha subunit Alpha 1 (CD49a) variant A domain. Note: This
CC variant sequence is not featured in the specification but has been
CC derived from the wild-type protein shown in AAU76851
XX
XX Sequence 195 AA;
XX
Query Match 40.7%; Score 417; DB 5; Length 195;
Best Local Similarity 45.5%; Pred. No. 3e-39;
Matches 80; Conservative 34; Mismatches 62; Indels 0; Gaps 0;
QY 23 CPTVMDVIVLDGNSIYPSEVOTFLRLVGLKLPIDPEQIQVCLVOYGSPPVHWSLGD 82
DB 1 CSTQLDIVLDGNSIYPMSVTFALNLLKRWMDIGKQIQVGIQVGENVTHEFWLNK 60
QY 83 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTGFSQSHGGRPEAARLLVVVTDGSHD 142
DB 61 YSSTEVLVAAKIVQGRGRQTMALGTDRTARKEAFTGARGGVKKVMVIVTDGSHD 120
QY 143 GEELPALKACEAGRVTRYGIYLVGLHYLRQRDPSSFLREIRTTASDPDERFFNV 198

Db 121 NHRLKKVIQCEDENLQRFSAIILGSYNRGNLSTKFXVELKSIASEPTEKHFFNV 176
RESULT 13
ADR23226
ID ADR23226 standard; protein; 198 AA.
XX AC ADR23226;
XX 04-NOV-2004 (first entry)
XX Human integrin CD49b alpha subunit A domain.
DE Human; integrin; CD49b; inflammation; antiinflammatory; vasotropic.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Domain 1. .195 /label = A_domain
FT Misc-difference 193 /note= "Invariant Ile residue"
FT
XX WO2004066914-A2.
PN 12-AUG-2004.
XX 12-MAY-2003; 2003WO-US014919.
XX 10-MAY-2002; 2002US-00144259.
PR (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout MA, Li R, Xiong J;
PI WPI; 2004-593980/57.
DR GENBANK; NP_002194.
XX
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
PT determining candidate compound for binding to CD11b, and for determining
PT compound as activation-dependent ligand.
XX
XX Disclosure; SEQ ID NO 6; 128pp; English.
XX
XX The present sequence is that of the human integrin alpha subunit CD49b A
CC domain. This includes an invariant Ile residue. The invention features a
CC variant integrin alpha subunit polypeptides in which the invariant Ile is
CC substituted by Gly, Ala or some other amino acid (e.g. Val) or is
CC deleted. The polypeptide can include part or all of the A domain.
CC Replacing the invariant Ile creates a variant integrin polypeptide that
CC is more active (i.e. in solution has a greater proportion of ligand-
CC forming polypeptides) than the wild-type form of the subunit. Variant
CC integrin polypeptides of the invention are useful in assays for compounds
CC that bind to a variant ligand, that interfere with or enhance the binding
CC of an integrin ligand to integrin, and for identifying activation-
CC specific ligands. They are also useful for generating antibodies, e.g.
CC monoclonal antibodies which bind to the high efficiency form of an
CC integrin. Some such antibodies recognise an epitope that is either not
CC present or not accessible on an integrin that is in a lower affinity
CC conformation. The invention also provides methods of administering a
CC variant integrin polypeptide, or an antibody that selectively binds it,
CC to identify a ligand which binds to an active integrin. Such assays are
CC useful for diagnosing inflammation, e.g. occult inflammation (e.g.
CC abscess or an active arteriosclerotic lesion). Variant integrin
CC polypeptides can also be used to affect the bioavailability of a variant
CC integrin polypeptide ligand and to treat disorders associated with
CC aberrant or unwanted integrin expression or activity, such as vascular
CC injury.
XX
XX Sequence 198 AA;
XX
Query Match 38.9%; Score 399; DB 8; Length 198;
Best Local Similarity 46.0%; Pred. No. 3.6e-37;

Matches 81; Conservative 29; Mismatches 66; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTLRLVGLKLFIDPEQIQVGLVQGESPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

Qy 83 FRTKEEVVRAAKNLSRREGRTKTAQAQIMVACTEGFSQSHGGRPEARLLVVVTDGSHD 142
 Db 61 YKTEEMIVATSQTSQYGGDLTNTFGAIQYARKVAYSASGGRSAAATKVMVWVTDGSHD 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFENV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKALIASIPTEYFFENV 176

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFENV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKALIASIPTEYFFENV 176

RESULT 14
 ID ABP54908 standard; protein; 198 AA.
 AC ABP54908;
 XX
 DT 08-JAN-2003 (first entry)
 DE Integrin alpha-2 I domain.
 KW Anthrax; toxin; receptor; integrin; human; antibacterial.
 OS Homo sapiens.
 FN WO200246228-A2.
 PD 13-JUN-2002.
 PF 03-OCT-2001; 2001WO-US030941.
 PR 05-DEC-2000; 2000US-0251481P.
 XX (WISC) WISCONSIN ALUMNI RES FOUND.
 PI Young JAT, Bradley KA, Collier RJ, Mogridge JS;
 XX WPI; 2002-713235/77.
 XX
 PT Novel isolated polypeptide useful for identifying agent that prevents or
 PT reduces effect of anthrax toxin on host cell, for treating human or non-
 PT human animal suffering from anthrax.
 XX
 PS Disclosure; Page 31-32; 45pp; English.
 XX
 CC The present sequence is the I domain of human integrin alpha-2. Ligand
 CC binding through I domains requires an intact metal ion-dependent adhesion
 CC site (MIDAS) motif. A MIDAS motif has been identified in the
 CC extracellular domain of a newly identified human anthrax toxin receptor
 CC (ATR). The invention provides ATR polypeptides (see ABP54903-06) and
 CC polynucleotides (see ABV73881), vectors, host cells, and transgenic and
 CC knock-out animals. It also provides methods for identifying molecules
 CC that bind the ATR and which reduce the toxicity of anthrax toxin. A
 CC claimed method for treating anthrax in a human or animal involves
 CC administering an agent that inhibits binding between PA and ATR at a
 CC level effective to reduce the severity of anthrax. Suitable agents
 CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at
 CC least 80% identical to these, a fusion protein, a monoclonal or
 CC polyclonal antibody, a polysaccharide, a lipid or a nucleic acid
 XX
 SQ Sequence 198 AA;

Query Match 38.3%; Score 393; DB 5; Length 198;
 Best Local Similarity 46.0%; Pred. No. 1.8e-36;
 Matches 81; Conservative 28; Mismatches 67; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTLRLVGLKLFIDPEQIQVGLVQGESPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

Qy 83 FRTKEEVVRAAKNLSRREGRTKTAQAQIMVACTEGFSQSHGGRPEARLLVVVTDGSHD 142
 Db 61 YKTEEMIVATSQTSQYGGDLTNTFGAIQYARKVAYSASGGRSAAATKVMVWVTDGSHD 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFENV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKALIASIPTEYFFENV 176

RESULT 15
 ID AAU76852 standard; protein; 195 AA.
 AC AAU76852;
 XX
 DT 21-MAY-2002 (first entry)
 DE Human integrin alpha subunit Alpha 2 (CD49b) A domain.
 KW Human; integrin alpha subunit; A domain; CD49b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 2;
 KW antiinflammatory; vasotropic; antiparasitic; pulmonary; gene therapy.
 OS Homo sapiens.
 FN WO200209737-A1;
 PD 07-FEB-2002.
 PF 31-JUL-2001; 2001WO-US023957.
 PR 31-JUL-2000; 2000US-0221950P.
 PR 11-JAN-2001; 2001US-00758493.
 PR 13-MAR-2001; 2001US-00805354.
 XX (GEO) GEN HOSPITAL CORP.
 PI Arnaout AM, Li R, Xiong J;
 XX WPI; 2002-188687/24.
 XX
 PT Novel high affinity integrin polypeptide useful for treating restenosis
 PT and parasitic diseases, comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.
 XX
 PS Example 2; Fig 5; 55pp; English.
 XX

CC The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit Alpha 2 (CD49b) A domain
 XX
 SQ Sequence 195 AA;

Query Match 38.0%; Score 389; DB 5; Length 195;
 Best Local Similarity 44.9%; Pred. No. 5.1e-36;
 Matches 79; Conservative 30; Mismatches 67; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTLRLVGLKLFIDPEQIQVGLVQGESPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

Db 1 CPSLIDVVVVCDESNSIYPWDVAVKNFLEKFVQGLDIGFTKTQVGLIQYANNPRVVFNLNT 60
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTEGFSQSHGGRPEAAARLLVVVTDGESH 142
Db 61 YKTKEEMIVATSQTSQYCGDLTNIFGAIQYARKYAYSAASGGRSATAKVMVVVTDGKSH 120
Qy 143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFPNV 198
Db 121 GSKLKAVIDQCNDHNDILRFGIAVLGYLNRNALDTKNLIKAIASIPTERYPFNV 176

Search completed: April 6, 2005, 14:36:34
Job time : 180 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:37:40 ; Search time 138 Seconds
(without alignments)
476.344 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQCSLAPTA.....FLRIRTIASDPDRFFNV 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 839692

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	912	89.0	195	10	US-09-805-354-7
2	912	89.0	195	11	US-09-758-493-7
3	912	89.0	195	14	US-10-144-259-7
4	492	48.0	193	10	US-09-805-354-8
5	492	48.0	193	11	US-09-758-493-8
6	492	48.0	193	14	US-10-144-259-8
7	427	41.7	195	10	US-09-805-354-5
8	427	41.7	195	11	US-09-758-493-5
9	427	41.7	195	14	US-10-144-259-5
10	424	41.4	192	15	US-10-474-832-59
11	424	41.4	192	15	US-10-474-832-61
12	419	40.9	192	15	US-10-346-863-57
13	419	40.9	192	15	US-10-474-832-60

14	399	38.9	195	10	US-09-805-354-6	Sequence 6, Appli
15	399	38.9	195	11	US-09-758-493-6	Sequence 6, Appli
16	399	38.9	195	14	US-10-144-259-6	Sequence 6, Appli
17	285.5	27.9	148	9	US-09-764-870-284	Sequence 284, App
18	285.5	27.9	148	9	US-09-764-870-444	Sequence 444, App
19	285.5	27.9	148	14	US-10-125-540-284	Sequence 284, App
20	285.5	27.9	148	14	US-10-125-540-444	Sequence 444, App
21	282	27.5	103	9	US-09-764-870-472	Sequence 472, App
22	282	27.5	103	11	US-09-764-875-1193	Sequence 1193, App
23	282	27.5	103	14	US-10-125-540-472	Sequence 472, App
24	244	23.8	176	10	US-09-976-782-38	Sequence 78, Appl
25	191	18.6	176	15	US-10-004-378A-79	Sequence 39, Appl
26	179	17.5	178	15	US-10-346-863-43	Sequence 43, Appl
27	179	17.5	180	15	US-10-346-863-31	Sequence 31, Appl
28	177.5	17.3	192	10	US-09-805-354-9	Sequence 9, Appli
29	177.5	17.3	192	11	US-09-758-493-9	Sequence 9, Appli
30	177.5	17.3	192	14	US-10-144-259-9	Sequence 9, Appli
31	175	17.1	150	15	US-10-346-863-30	Sequence 30, Appl
32	175	17.1	180	15	US-10-080-334-130	Sequence 130, App
33	172.5	16.8	180	15	US-10-346-863-40	Sequence 40, Appl
34	163	15.9	176	15	US-10-004-378A-81	Sequence 81, Appl
35	156	15.2	191	10	US-09-805-354-3	Sequence 3, Appli
36	156	15.2	191	11	US-09-758-493-3	Sequence 3, Appli
37	156	15.2	191	14	US-10-144-259-3	Sequence 3, Appli
38	150	14.6	166	15	US-10-074-978A-265	Sequence 265, App
39	148	14.4	182	15	US-10-346-863-33	Sequence 33, Appl
40	148	14.4	182	15	US-10-346-863-35	Sequence 35, Appl
41	148	14.4	182	15	US-10-346-863-36	Sequence 36, Appl
42	148	14.4	183	15	US-10-346-863-20	Sequence 20, Appl
43	148	14.4	183	15	US-10-346-863-41	Sequence 41, Appl
44	148	14.4	183	16	US-10-615-515-7	Sequence 7, Appli
45	148	14.4	184	10	US-09-805-354-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-805-354-7
; Sequence 7, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xi, Jiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-805-354-7

Query Match 89.0%; Score 912; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	23	CPTVMDVVILVDGNSIYPWSEVQTFRLRLVKGKLFIDPEQIQVGLVOYGESPVHWSIGD	82
Db	1	CPTVMDVVILVDGNSIYPWSEVQTFRLRLVKGKLFIDPEQIQVGLVOYGESPVHWSIGD	60
Qy	83	FRTEEVVRAAKNLSRREGRETKTQAQIMVACTEGFSQSHGGRPEARLLVVVTDGESH	142
Db	61	FRTEEVVRAAKNLSRREGRETKTQAQIMVACTEGFSQSHGGRPEARLLVVVTDGESH	120

```
Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 2
US-09-758-493-7
; Sequence 7, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-7

Query Match 89.0%; Score 912; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 3
US-10-144-259-7
; Sequence 7, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-7

Query Match 89.0%; Score 912; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 4
US-09-805-354-8
; Sequence 8, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-8

Query Match 48.0%; Score 492; DB 10; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLDPQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 YRSKDVVEAAASHIEQRGGTETRTAFGIEFARSEAFQK--GGRKGAKKVMIVITDGESH 118

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 119 SPDLKVIQSERDNTVRYAVAVLGYNNRRGINPETFLNEIKYIASDPDDKHFFNV 174

RESULT 5
US-09-758-493-8
; Sequence 8, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-8

Query Match      48.0%; Score 492; DB 11; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CQTYMDIVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YRSVKDVVEAAASHLEQGGTETRTAFGLFEPARSAFQK--GGRGAKKVMIVITDGSND 118
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTRYGIYGLVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SPDLEKVIQOSERDNTVYAVAVLGYNNRGINPETFLNEIKYIASDDDDKHFFNV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-10-144-259-8
; Sequence 8, Application US/10144259
; Publication No. US20030105691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-8

Query Match      48.0%; Score 492; DB 14; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CQTYMDIVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YRSVKDVVEAAASHLEQGGTETRTAFGLFEPARSAFQK--GGRGAKKVMIVITDGSND 118
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTRYGIYGLVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SPDLEKVIQOSERDNTVYAVAVLGYNNRGINPETFLNEIKYIASDDDDKHFFNV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-805-354-5
; Sequence 5, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
```

```
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-5

Query Match      41.7%; Score 427; DB 10; Length 195;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CSTQLDIVIVLDGNSIYPWDSVTAFLNDLLKRMIDIGPKQTQVGIQYGENVTHEFNLNK 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YSSTEELVAAKKIVQGGRTMTALGTDTRARKEAFTEARGARRGVKKVMVIVTDGSHD 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTRYGIYGLVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NHRLLKKVIQDCEDENIQRFSAIILGNSYRNLSTKTEKFVEEIKSIASEPTEKHFFNV 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-758-493-5
; Sequence 5, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-5

Query Match      41.7%; Score 427; DB 11; Length 195;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CSTQLDIVIVLDGNSIYPWDSVTAFLNDLLKRMIDIGPKQTQVGIQYGENVTHEFNLNK 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YSSTEELVAAKKIVQGGRTMTALGTDTRARKEAFTEARGARRGVKKVMVIVTDGSHD 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTRYGIYGLVGLHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NHRLLKKVIQDCEDENIQRFSAIILGNSYRNLSTKTEKFVEEIKSIASEPTEKHFFNV 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-144-259-5
; Sequence 5, Application US/10144259
```


[illegible]

This page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:29:18 ; Search time 43 Seconds
(without alignments)
343.733 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337

Perfect score: 1025

Sequence: 1 GICARVDASFPQGS LAPTA.....FLREIRTIASDPDERFFNV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 392136

Minimum DB seq length: 0

Maximum DB seq length: 198

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	14.4	181	5	PCT-US96-01314-61
2	148	14.4	184	3	US-08-974-899-7
3	148	14.4	184	4	US-09-795-798-7
4	147	14.3	187	2	US-08-177-109A-62
5	147	14.3	187	2	US-08-687-706-62
6	147	14.3	187	5	PCT-US96-01314-60
7	145	14.1	184	3	US-08-974-899-8
8	145	14.1	184	4	US-09-795-798-8
9	144	14.0	187	2	US-08-177-109A-61
10	144	14.0	187	2	US-08-687-706-61
11	93	9.1	187	3	US-08-463-682-1
12	73	7.1	77	4	US-09-513-999C-6277
13	69	6.7	167	4	US-09-252-991A-21325
14	69	6.7	176	4	US-09-704-139-2
15	68.5	6.7	177	4	US-09-252-991A-29795
16	68.5	6.7	191	4	US-09-902-540-10334
17	68	6.6	188	4	US-09-902-540-10761
18	67.5	6.6	45	1	US-08-462-128-38
19	67.5	6.6	45	1	US-08-463-180-38
20	66	6.4	164	4	US-09-902-540-9764
21	65	6.3	190	4	US-09-134-000C-4833
22	64.5	6.3	180	4	US-09-904-615-78
23	64	6.2	178	4	US-09-270-767-36123
24	64	6.2	178	4	US-09-270-767-51340
25	64	6.2	182	4	US-09-270-767-61623
26	64	6.2	184	4	US-09-328-352-5086
27	63.5	6.2	85	1	US-08-341-219-22

Sequence 22, Appl
Sequence 12480, A
Sequence 683, App
Sequence 7548, A
Sequence 3643, Ap
Sequence 16942, A
Sequence 57892, A
Sequence 58950, A
Sequence 3, Appl
Sequence 62180, A
Sequence 4391, A
Sequence 32498, A
Sequence 47715, A
Sequence 4813, Ap
Sequence 12386, A
Sequence 16670, A
Sequence 32444, A
Sequence 15448, A

28 63.5 6.2 85 3 US-08-912-314A-22
29 63 6.1 169 4 US-09-902-540-12480
30 62.5 6.1 121 4 US-09-640-211A-683
31 62 6.0 147 4 US-09-543-681A-7548
32 62 6.0 153 4 US-09-540-236-3643
33 61 6.0 193 4 US-09-252-991A-16942
34 61 6.0 193 4 US-09-270-767-57892
35 61 6.0 193 4 US-09-270-767-58950
36 60.5 5.9 75 3 US-08-864-357F-3
37 60.5 5.9 81 4 US-09-270-767-62180
38 60.5 5.9 164 4 US-09-107-532A-4391
39 60 5.9 140 4 US-09-270-767-32498
40 60 5.9 140 4 US-09-270-767-47715
41 59.5 5.8 149 4 US-09-513-999C-4813
42 59 5.8 112 4 US-09-902-540-12386
43 59 5.8 157 4 US-09-902-540-16670
44 59 5.8 190 4 US-09-252-991A-32444
45 59 5.8 195 4 US-09-902-540-15448

ALIGNMENTS

RESULT 1
PCT-US96-01314-61
; Sequence 61, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaut
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01314-61

Query Match 14.4%; Score 148; DB 5; Length 181;
Best Local Similarity 25.4%; Pred. No. 3e-10;
Matches 44; Conservative 37; Mismatches 70; Indels 22; Gaps 6;
Qy 27 MDVVILVDGMSIYP--WSEVQTFLRLVGLKFLFDPEQIQVGLVQVGSPPVHWSLGF- 83
Db 6 VDLVFLFDGMSLQPDFFQKILDFMKVKKL--SNTSYQFAAVQFSTSYKTFDFSDYV 63

Qy	84	--RTKEVVVRAAKNLSRREGRET	TKTAQIMVACTEGFSQSHGSRPEARL	VLVVVTDGESH	141
Db	64	KWKDPDALLKHVKHMLL	-----TTTFGAINVATEVFREELGAR	PDATKVLIITDGEAT	119
Qy	142	DGEELPAALKACEAGRVTRYGI	ALVGHYLRQRDPSSFLEIRTI	IASDPPDERP	194
Db	120	DGNGIDAAND-----IIRYIIGIK	HPOTKESOE	-----LHKFASKPASEP	161

RESULT 2

```

US-08-974-899-7
; Sequence 7, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

```

Query Match	14.4%	Score 148;	DB 3;	Length 184;
Best Local Similarity	25.4%	Pred. No. 3.1e-10;		
Matches 44;	Conservative	37;	Mismatches 70;	Gaps 6;
			Indels 22;	

84	Qy	--RTKEVVR	AAKNU	SRREGRET	TKTAQ	IAVM	ACTEG	FSQSHG	RPEAR	LLVVVT	QESH	141
62	Db	KKKOPD	ALLK	VYKMLL	-----	TNTF	GAINT	VATE	VEFREL	GARP	DTKVLII	117
142	Qy	DGEEL	PAAL	KACE	AGRV	TRYGI	AVLGH	YLRQR	DPSSF	ELREIT	IASD	194
118	Db	DSGNIDA	AKD	-----	IIRY	IIGIK	FPQTK	ESQET	-----	LHKF	ASKP	159

RESULT 3

US-09-795-798-7
; Sequence 7, Application US/09795798
; Patent No. 6703018

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

Query Match	14.4%	Score 148;	DB 4;	Length 184;
Best Local Similarity	25.4%	Pred. No. 3.1e-10;		
Matches 44; Conservative	37;	Mismatches 70;	Indels 22;	Gaps 6;

84	QY	--RTKEVVRAAKNLSRREGRETTIAQAIIWACTEFGSQSHGGRPENARLLVVTGDESH	141
62	Db	KKKDPDALLKHVKHMLL-----TNTPGAINVATVEFRELGGARPDAKTVLIIITDGEAT	117
142	QY	DGEELPAALKAACEAGRVTRYGIALGHLYLRQRDPSPFLREIRTIASDDPERF	194
118	Db	DSGNIDAAKD-----IIRYIGIGKGHFQTKESOET-----LHKFPASKPASEF	159

RESULT 4

US-08-177-109A-62
; Sequence 62, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-463-682-1

Query Match 9.1%; Score 93; DB 3; Length 187;
Best Local Similarity 20.7%; Pred. No. 0.0029;
Matches 38; Conservative 46; Mismatches 72; Indels 28; Gaps 6;
Qy 23 CPTVMDVVIVLDGNN--SIYPWSEVOTFLRLVGLKFLDPQIOVGLVQVGESPFHWSL 80
Db 1 CSRLLDLVFLDGGSRSEAEFEVLFKAPVVDMMERLRISQKWVAVVVEYHDGSHAYIGL 60
Qy 81 GDFRTKEEVRRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGES 140
Db 61 KDKRPSRLRIASQVKYAGSQVASTSEVLKVTYLFQIFSKI--DRPEASRIALLL----- 113
Qy 141 HDGELPALKACAGRVTRYGVIAVLGHLRRQR-----DPSFLEIRTTASD-PD 191
Db 114 -----MASQSPQMRNFRVYV-QGLKKKKVIVIPVGIGPHANLKQIRLIEKOAPE 163
Qy 192 ERF 195
Db 164 NKA 167

RESULT 12
US-09-513-999C-6277
Sequence 6277, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6277
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 66
OTHER INFORMATION: Xaa=Cys or Gly
US-09-513-999C-6277

Query Match 7.1%; Score 73; DB 4; Length 77;
Best Local Similarity 40.0%; Pred. No. 0.25;
Matches 16; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
Qy 103 ETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
Db 3 DTHGLALVYAKELQFAEASGARPGVPKVLVWVTDGSSD 42

RESULT 13
US-09-252-991A-21325
Sequence 21325, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21325
LENGTH: 167
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21325

Query Match 6.7%; Score 69; DB 4; Length 167;
Best Local Similarity 38.7%; Pred. No. 2.7;
Matches 29; Conservative 3; Mismatches 31; Indels 12; Gaps 3;
Qy 90 VRAAKNLSRREGRETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDG----- 143
Db 1 VMANEOKRDEGVIEKLQVNRVAKT-----VKGRIFAFPTALTVVGDGKRVGFRGKA 55
Qy 144 EELPAL-KACEAGR 157
Db 56 REVPAIQKAMEAAR 70

RESULT 14
US-09-704-139-2
Sequence 2, Application US/09704139
Patent No. 6420153
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosanna
TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
FILE REFERENCE: 10448-018001
CURRENT APPLICATION NUMBER: US/09/704,139
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/185,772
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1390)
OTHER INFORMATION: n = a, t, g, or c
US-09-704-139-2

Query Match 6.7%; Score 69; DB 4; Length 176;
Best Local Similarity 28.0%; Pred. No. 2.9;
Matches 37; Conservative 17; Mismatches 50; Indels 28; Gaps 7;
Qy 89 VVRAAKNL-----SRREGRETKTAQAIMVACTEGFSQSHGGR-PEAARLLVVVTDGESHD- 142
Db 19 LVRVAPSLFLGSAAGAEQLARAGVTLCNVNSRQGPAPGVAELRVFVDDPAEDL 78
Qy 143 -----GEELPAALKA-----CEAGRVTRYGVIAVLGHLRRORDPS-----SPUREI 183
Db 79 LAHLEPTCAAMEAAVRAAGGACLVCKNGR--SRSAVCTAYLWMHRLSLAKAFQWVKA 136
Qy 184 RTIASDPDERFF 195

Db 137 RPVA-EPNPGFW 147

RESULT 15

US-09-252-991A-29795
; Sequence 29795, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29795
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29795

Query Match 6.7%; Score 68.5; DB 4; Length 177;
Best Local Similarity 24.0%; Pred. No. 3.4;
Matches 37; Conservative 14; Mismatches 62; Indels 41; Gaps 6;
Qy 67 LVQYGESPVHEWSLGDPR-----KEEVVRAAKNLSRRE-----GRETKT 106
Db 28 LPRGARPTPRGLGGTTIOPDTALLEQQGVLLKKATARCVAQAGRGGAAGPAGAPDRG 87
Qy 107 AQAIMVACTEG-----FSQSHGGRPEAAKLLVVVTGESH-----GEELPAALKACEAGRVT 159
Db 88 ARGGRCRCPGGRPTLYPAGGARDPR-----SEGRGNDPGGGELGAAQRLPGLG--- 139
Qy 160 RYGIATVGHYLRORDPSSFLREIRTTIASDPDR 193
Db 140 -----LAHQLRRRRAPALRVALLRQOQQPDHR 167

Search completed: April 6, 2005, 14:41:28
Job time : 49 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:33:34 ; Search time 42 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986
Perfect score: 192
Sequence: 1 YEVHPYGLPVGPGPEFKTLRVQNLGCVVSGLI 35

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 7756

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	19.3	35	2	PC2297
2	36	18.8	26	2	S05414
3	35.5	18.5	33	2	S13863
4	35	18.2	33	2	D61563
5	35	18.2	35	2	A34257
6	34.5	18.0	35	2	B36912
7	34	17.7	35	2	PC2295
8	33	17.2	10	2	H60588
9	33	17.2	30	2	I69492
10	32	16.7	22	2	P00070
11	32	16.7	30	2	S74112
12	32	16.7	35	2	PC2296
13	32	16.7	35	2	B41161
14	31.5	16.4	35	2	AD2525
15	31	16.1	19	2	S68394
16	31	16.1	20	2	A36016
17	31	16.1	24	2	T42441
18	31	16.1	24	2	B30609
19	31	16.1	28	2	A31859
20	31	16.1	28	2	JN0366
21	31	16.1	34	2	C31514
22	30.5	15.9	35	2	PC2294
23	30.5	15.9	35	2	S18264
24	30	15.6	18	2	C32537
25	30	15.6	20	2	PL0161
26	30	15.6	22	2	D32537
27	30	15.6	27	2	C54257
28	30	15.6	28	2	S41774
29	30	15.6	28	2	I48349

30 30 15.6 33 2 A95047
31 30 15.6 34 2 H95019
32 30 15.6 35 2 PC2293
33 29.5 15.4 27 2 A24487
34 29 15.1 15 2 S08282
35 29 15.1 22 2 A39269
36 29 15.1 27 2 S64717
37 29 15.1 30 2 A34874
38 29 15.1 35 2 PC2298
39 28.5 14.8 33 2 A60507
40 28 14.6 19 2 S69153
41 28 14.6 20 2 S65399
42 28 14.6 20 2 PU0033
43 28 14.6 22 2 H30608
44 28 14.6 25 2 S36378
45 28 14.6 26 2 G30608

hypothetical prote
hypothetical prote
V3 domain peptide
aldose 1-epimerase
cytochrome P450K-2
LX-1 tumor antigen
formin binding pro
transforming prote
V3 domain peptide
pepsin I (EC 3.4.2
Neb-collagenase
immunodeficiency v
aldose 1-epimerase
Ig kappa chain V-I
Ig heavy chain V r
Ig kappa chain V-I

ALIGNMENTS

RESULT 1

PC2297
V3 domain peptide P4611 - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: PC2297
R:Sherefa, K.; Soenmerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A:Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
A:Reference number: PC2291; MUID:95110306; PMID:7811250
A:Accession: PC2297
A:Molecule type: protein
A:Residues: 1-35 <SHE>
A:Cross-references: UNIPROT:Q77729
C:Superfamily: type B retrovirus env polyprotein

Query Match 19.3%; Score 37; DB 2; Length 35;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTT 20
Db 11 SIPIGGRALYTT 23

RESULT 2

S05414
steryl-sulfatase (EC 3.1.6.2), microsomal - rat (fragment)
N:Alternate names: arylsulfatase C
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Apr-1993
C:Accession: S05414
R:Kawano, J.I.; Kotani, T.; Ohtaki, S.; Minamino, N.; Matsuo, H.; Oinuma, T.; Aikawa, E.
Biochim. Biophys. Acta 997, 199-205, 1989
A:Title: Characterization of rat and human steroid sulfatases.
A:Reference number: S05414; MUID:89352671; PMID:2765556
A:Accession: S05414
A:Molecule type: protein
A:Residues: 1-26 <KAW>
C:Keywords: sulfuric ester hydrolase

Query Match 18.8%; Score 36; DB 2; Length 26;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 12 GPGEPEF-----KTLRVQNLGCV 29
Db 4 GPGFNFLIMADDLIGDLGXY 25

RESULT 3

S13863

dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Trypanosoma cruzi (fragment)
C/Species: Trypanosoma cruzi
C/Date: 18-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 23-May-1997
C/Acession: S13863
R/Lohrer, H.; Krauth-Siegel, R.L.
Eur. J. Biochem. 194, 863-869, 1990
A/Title: Purification and characterization of liposome dehydrogenase from Trypanosoma
A/Reference number: S13863; MUID:91099369; PMID:2269305
A/Acession: S13863
A/Molecule type: protein
A/Residues: 1-33 <LO>
C/Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
C/Keywords: FAD; flavoprotein; homodimer; lipoamide; NAD; oxidoreductase; redox-active d
F;4-32/Region: beta-alpha-beta FAD nucleotide-binding fold

Query Match 18.5%; Score 35.5; DB 2; Length 33;
Best Local Similarity 31.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 11; Gaps 1;

Qy 4 HPVGTPLVGPGPEFKTTLRVQLGCVVS 32
: : : : :
Db 1 NPVDVVIGGP-----GGYVAS 18

RESULT 4

D61563
neurophysin 1 - chicken (fragments)
C/Species: Gallus gallus (chicken)
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C/Acession: D61563
R/Levy, B.; Michel, G.; Chauvet, J.; Chauvet, M.T.; Acher, R.
BioSci. Rep. 7, 631-636, 1987
A/Title: Gene conversion in avian mesotocin and vasotocin genes: a recurrent mechanism
A/Reference number: A61563; MUID:88108074; PMID:3427215
A/Acession: D61563
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-33 <LEV>
A/Cross-references: UNIPROT:O7LZN7
C/Superfamily: oxytocin-neurophysin
C/Keywords: hormone

Query Match 18.2%; Score 35; DB 2; Length 33;
Best Local Similarity 37.0%; Pred. No. 3.1e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 8; Gaps 2;

Qy 9 LPVGP-----GPEFKTTLRVQLGCVV 30
: : : : :
Db 3 LPCGPRNKCFGNICG---EELGCYL 26

RESULT 5

A54257
deoxyribose kinase complex I S-component - Lactobacillus acidophilus (fragment)
C/Species: Lactobacillus acidophilus
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Acession: A54257
R/Ikeda, S.; Ma, G.T.; Ives, D.H.
Biochemistry 33, 5328-5334, 1994
A/Title: Heterodimeric deoxyribonucleoside kinases of Lactobacillus acidophilus R-26; functi
A/Reference number: A54257; MUID:94227067; PMID:8172906
A/Acession: A54257
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-35 <IKE>
A/Cross-references: UNIPROT:Q9R4Z3
A/Experimental source: R-26
A/Note: sequence extracted from NCBI backbone (NCBIP:146748)
C/Superfamily: Lactobacillus acidophilus deoxyadenosine kinase

Query Match 18.2%; Score 35; DB 2; Length 35;
Best Local Similarity 38.9%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Query Match 17.2%; Score 33; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GTLPVGP 14
| | | | |
DB 1 GTLPVGP 8

RESULT 9
I69492
gene aeg-46.5 protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I69492
R:Choe, M.; Reznikoff, W.S.
J. Bacteriol. 175, 1165-1172, 1993
A:Title: Identification of the regulatory sequence of anaerobically expressed locus aeg-46.5
A:Reference number: I54984; MUID:93163046; PMID:8432709
A:Accession: I69492
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-30 <REG>
A:Cross-references: UNIPROT:Q53301; GB:S54754; NID:g265388; PIDN:AAB25330.1; PID:g265389

Query Match 17.2%; Score 33; DB 2; Length 30;
Best Local Similarity 31.4%; Pred. No. 5.4e+02;
Matches 11; Conservative 2; Mismatches 4; Indels 18; Gaps 2;

QY 3 VHPVG-----TLVPVGPGEFKTTLRVQNL 26
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MHPVGAYSLVAGAKPVTVSRPGP-----VMNL 28

RESULT 10
PQ0070
T-cell receptor beta chain (BTB15) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0070
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0070
A:Molecule type: mRNA
A:Residues: 1-22 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB15
C:Keywords: receptor

Query Match 16.7%; Score 32; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 YGTLVGP 14
| | | | |
DB 8 YGELHFGP 16

RESULT 11
S74112
proline-rich antibacterial protein - green crab (fragment)
C:Species: Carcinus maenas (green crab, common shore crab)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C:Accession: S74112
R:Schnapp, D.; Kemp, G.D.; Smith, V.J.
Eur. J. Biochem. 240, 532-539, 1996
A:Title: Purification and characterization of a proline-rich antibacterial peptide, with
A:Reference number: S74112; MUID:97008941; PMID:8856051
A:Accession: S74112
A:Molecule type: protein

A:Residues: 1-30 <SCH>
A:Cross-references: UNIPROT:P82964
A:Experimental source: haemocytes
C:Keywords: antibacterial

Query Match 16.7%; Score 32; DB 2; Length 30;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PYGTLPVGP 15
| | | | |
DB 8 PPRPPGPRP 18

RESULT 12
PC2296
V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: PC2296
R:Sherefa, K.; Soennerborg, A.; Steinberg, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A:Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping
A:Reference number: PC2291; MUID:95110306; PMID:7811250
A:Accession: PC2296
A:Molecule type: protein
A:Residues: 1-35 <SHE>
A:Cross-references: UNIPROT:Q70826; UNIPROT:Q70831
C:Superfamily: type E retrovirus env polyprotein

Query Match 16.7%; Score 32; DB 2; Length 35;
Best Local Similarity 46.2%; Pred. No. 8.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 TLPVGPGEPEFKTT 20
| | | | | | | | | | | | | | | | | | | | |
DB 11 SIHMGPGRAFTT 23

RESULT 13
B41161
29K antigen PEB2 - Campylobacter jejuni (fragment)
C:Species: Campylobacter jejuni
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C:Accession: B41161
R:Pei, Z.; Ellison III, R.T.; Blaser, M.J.
J. Biol. Chem. 266, 16363-16369, 1991
A:Title: Identification, purification, and characterization of major antigenic proteins
A:Reference number: A41161; MUID:91358413; PMID:1885571
A:Accession: B41161
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-35 <PEI>
A:Cross-references: UNIPROT:Q9R5T9

Query Match 16.7%; Score 32; DB 2; Length 35;
Best Local Similarity 47.1%; Pred. No. 8.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 2 EVHPYGTLPVGPGEPEFK 18
| | | | | | | | | | | | | | | | | | | | |
DB 1 EILVYG--PGGPAPVLK 15

RESULT 14
AD2525
hypochemical protein asr7380 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2525
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-35 <KUR>
A;Cross-references: UNIPROT:Q8YKCL; GB:BA000020; PIDN:BA077138.1; PID:g17134579; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr7380
A;Genome: plasmid

Query Match 16.4%; Score 31.5; DB 2; Length 35;
Best Local Similarity 40.7%; Pred. No. 1e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 13; Gaps 2;

Qy 11 VGPGEPEKTLRVQN-----LGC 28
||| |||||
Db 6 VGDG-----DTLRVRNQOQPITIRLGC 28

RESULT 15

S68394
H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii (fra
N;Alternate names: ATP synthase chain G
C;Species: Chlamydomonas reinhardtii
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S68394
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal
A;Reference number: S68388; MUID:96128220; PMID:8543042
A;Accession: S68394
A;Molecule type: protein
A;Residues: 1-19 <FIE>
A;Cross-references: UNIPROT:Q98882
A;Experimental source: strain CW15
C;Genetics:
A;Genome: nuclear
C;Keywords: chloroplast; hydrolase

Query Match 16.1%; Score 31; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EVHPYGTLPVGPGE 16
::: |||
Db 4 KIDFNTLPVNAGEE 18

Search completed: April 6, 2005, 13:46:20
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:10:34 ; Search time 180 Seconds
(without alignments)
99.571 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEVHPGTLVPVGPGEFKTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 37082

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	24.0	34	2	O91354 human immun
2	46	24.0	34	2	O91355 human immun
3	46	24.0	34	2	O91357 human immun
4	46	24.0	34	2	O78489 human immun
5	45	23.4	34	2	O78487 human immun
6	45	23.4	35	2	O90519 human immun
7	45	23.4	35	2	O91436 human immun
8	45	23.4	35	2	O91437 human immun
9	45	23.4	35	2	O76251 human immun
10	44	22.9	35	2	O10869 human immun
11	44	22.9	35	2	O91434 human immun
12	44	22.9	35	2	O91454 human immun
13	44	22.9	35	2	Q6W884 human immun
14	44	22.9	35	2	O76250 human immun
15	44	22.9	35	2	O76296 human immun
16	44	22.9	35	2	O80499 human immun
17	43	22.4	34	2	O91356 human immun
18	43	22.4	34	2	Q6GPQ3 human immun
19	43	22.4	34	2	Q70742 human immun
20	43	22.4	34	2	Q70743 human immun
21	43	22.4	34	2	Q70747 human immun
22	43	22.4	35	2	O90503 human immun
23	43	22.4	35	2	O91349 human immun
24	43	22.4	35	2	O91350 human immun
25	43	22.4	35	2	O91351 human immun
26	43	22.4	35	2	O91430 human immun
27	43	22.4	35	2	O91433 human immun
28	43	22.4	35	2	O91435 human immun
29	43	22.4	35	2	O91438 human immun
30	43	22.4	35	2	O91439 human immun
31	43	22.4	35	2	O91440 human immun

32	43	22.4	35	2	O91446	human immun
33	43	22.4	35	2	Q6W882	human immun
34	43	22.4	35	2	Q6W892	human immun
35	43	22.4	35	2	Q6W893	human immun
36	43	22.4	35	2	Q6W894	human immun
37	43	22.4	35	2	Q70232	human immun
38	43	22.4	35	2	Q76295	human immun
39	43	22.4	35	2	Q76PL9	human immun
40	43	22.4	35	2	Q76PM0	human immun
41	43	22.4	35	2	Q76PM1	human immun
42	43	22.4	35	2	Q76PM2	human immun
43	43	22.4	35	2	Q76PM3	human immun
44	43	22.4	35	2	Q76PM4	human immun
45	43	22.4	35	2	Q76PM5	human immun

ALIGNMENTS

RESULT 1

O91354	O91354	PRELIMINARY;	PRT;	34 AA.
AC	O91354;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Envelope glycoprotein (Fragment).			
GN	Name=env;			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98090117; PubMed=9430252;			
RA	Iga S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,			
RA	Kimura S., Iwamoto A., Oka S.;			
RT	"HIV type 1 V3 variation dynamics in vivo:long-term persistence of			
RT	non-syncytium-inducing genotypes and transient presence of syncytium-			
RT	inducing genotypes during the course of progressive AIDS.";			
RL	AIDS Res. Hum. Retroviruses 13:1597-1609(1997).			
DR	EMBL; AB005326; BAA3244.1;			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0019028; C:viral capsid; IEA.			
DR	GO; GO:0019031; C:viral envelope; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	InterPro; IPR00777; GP120.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00516; GP120; 1.			
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.			
FT	NON_TER	1		
FT	NON_TER	34		
SQ	SEQUENCE	34 AA; 3785 MW; A31972064FAD828F CRC64;		

Query Match 24.0%; Score 46; DB 2; Length 34;

Best Local Similarity 42.1%; Pred.No. 61; Mismatches 5; Indels 0; Gaps 0;

Matches 8; Conservative

Oy 8 TLPVGPGEFKTLRVQNL 26

Db 11 SIPIGPGAFYTTIIGNI 29

RESULT 2

O91355	O91355	PRELIMINARY;	PRT;	34 AA.
AC	O91355;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Envelope glycoprotein (Fragment).			
GN	Name=env;			
OS	Human immunodeficiency virus 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			


```

RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M92127; AAA4575.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3818 MW; A93F02E148C0428F CRC64;

Query Match 23.4%; Score 45; DB 2; Length 34;
Best Local Similarity 42.1%; Pred. No. 85;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRVQNL 26
Db 11 SIPMGPGAFYTTIIGNI 29

RESULT 6
ID O90519 PRELIMINARY; PRT; 35 AA.
AC O90519;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99211246; PubMed=10197389;
RA Vallejo A., Mas A., Heredia A., Altisent C., Lorenzo I., Soriano V.,
RA Hewlett I.K.;
RT "V3-loop and nef gene sequences of HIV-1 isolates from a hemophilic
RT cohort with long-term non-progressive infection.";
RL AIDS 13:532-534(1999).
DR EMBL; AF082373; AAC34519.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3878 MW; 9F5A59F6B78C81BE CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRV 23
Db 11 SIPMGPGAFYTTDRI 26

RESULT 7
ID O91436 PRELIMINARY; PRT; 35 AA.
AC O91436;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

```

```

GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-syctium-inducing genotypes and transient presence of cyncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
DR EMBL; AB005421; BAA33338.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3956 MW; 9F5A5B3A688BF77E CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 43.8%; Pred. No. 87;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRV 23
Db 11 SIPMGPGAFYTTROI 26

RESULT 8
ID O91437 PRELIMINARY; PRT; 35 AA.
AC O91437;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-syctium-inducing genotypes and transient presence of cyncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
DR EMBL; AB005422; BAA33339.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3956 MW; 9F5A5B3A688BF77E CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 43.8%; Pred. No. 87;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```



```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-synctium-inducing genotypes and transient presence of cyncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609 (1997).
DR EMBL: AB005440; BAA33356.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 1 35
SQ SEQUENCE 35 AA; 4026 MW; 9E4A4A3A688BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LPVGPGEPEFKTTLRV 23
Db 12 IPIGPGRAFYTTQI 26

RESULT 13
Q6W884
ID Q6W884 PRELIMINARY; PRT; 35 AA.
AC Q6W884;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GP120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22918189; PubMed=14554089; DOI=10.1016/S0042-6822(03)00464-1;
RA Kulkosky J., Sullivan J., Xu Y., Malin-Markham A., Otero M.,
RA Calarota S., Zielinski J., Culnan D.M., Pomerantz R.J.;
RT "Genotypic alteration of HAART-persistent HIV-1 reservoirs in vivo.";
RL Virology 314:617-629 (2003).
DR EMBL: AY305414; AAQ88346.1; -
DR InterPro: IPR000777; GP120.
DR InterPro: IPR011056; Pept_S24_S26_C.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 1 35
SQ SEQUENCE 35 AA; 3830 MW; 9F48FD8B88BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 TLPVGPGEPEFKT 20
Db 11 SIPIGPGKAFYTT 23

RESULT 14
Q76250
ID Q76250 PRELIMINARY; PRT; 35 AA.
AC Q76250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

```

```

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE V3 loop (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94246736; PubMed=8189527;
RA Schreiber M.G., Petersen H., Wachsmuth C., Muller H., Hufert F.T.,
RA Schmitz H.;
RT "Antibodies of symptomatic human immunodeficiency virus type 1-
RT infected individuals are directed to the V3 domain of noninfectious
RT and not of infectious virions present in autologous serum.";
RL J. Virol. 68:3908-3916 (1994).
DR EMBL: Z15163; CAA78862.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR011056; Pept_S24_S26_C.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 1 35
SQ SEQUENCE 35 AA; 3775 MW; 9F5B905B88BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LPVGPGEPEFKTTLRV 23
Db 12 IPIGPGRAFYTTQI 26

RESULT 15
Q76296
ID Q76296 PRELIMINARY; PRT; 35 AA.
AC Q76296;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE V3 loop (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94246736; PubMed=8189527;
RA Schreiber M.G., Petersen H., Wachsmuth C., Muller H., Hufert F.T.,
RA Schmitz H.;
RT "Antibodies of symptomatic human immunodeficiency virus type 1-
RT infected individuals are directed to the V3 domain of noninfectious
RT and not of infectious virions present in autologous serum.";
RL J. Virol. 68:3908-3916 (1994).
DR EMBL: Z15163; CAA78862.1; -
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000777; GP120.
DR InterPro: IPR011056; Pept_S24_S26_C.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 1 35
SQ SEQUENCE 35 AA; 3775 MW; 9F5B905B88BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LPVGPGEPEFKTTLRV 23
Db 12 IPIGPGRAFYTTQI 26

```

Qy 8 TLPVGPQPEFKTT 20
: : : : :
Db 11 SIPIGGSAFYTT 23

Search completed: April 6, 2005, 13:44:42
Job time : 181 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:08:44 ; Search time 168 Seconds
(without alignments)
80.575 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986
Perfect score: 192
Sequence: 1 YEHVPVGLTPVGPPEKTKTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 854512

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	24.0	33	2	AAR68713 PRI/T5 ch
2	46	24.0	33	2	AAR68713 Chimaeric
3	46	24.0	33	2	AAR68713 HIV-1 pep
4	46	24.0	33	2	AAR68713 HIV-1 vac
5	46	24.0	33	2	AAR68713 HIV-1 vac
6	46	24.0	33	2	AAR68713 HIV-1 vac
7	45.5	23.7	33	2	AAR68712 PRI/T5 ch
8	45.5	23.7	33	2	AAR68712 Chimaeric
9	45.5	23.7	33	2	AAR68712 HIV-1 pep
10	45.5	23.7	33	2	AAR68712 HIV-1 vac
11	45.5	23.7	33	2	AAR68712 HIV-1 vac
12	45.5	23.7	33	2	AAR68712 HIV-1 vac
13	44	22.9	24	2	AAR04467 Human imm
14	44	22.9	35	3	AAB10706 HIV-1 iso
15	44	22.9	35	5	ABG73686 HIV-1 V3-
16	43.5	22.7	33	2	AAR68710 PRI/P24H
17	43.5	22.7	33	2	AAR68710 Chimaeric
18	43.5	22.7	33	2	AAR68710 HIV-1 pep
19	43.5	22.7	33	2	AAR68710 HIV-1 vac
20	43.5	22.7	33	2	AAR68710 HIV-1 vac
21	43.5	22.7	35	2	AAR68710 HIV-1 vac
22	43	22.4	18	2	AAR68679 Consensus
23	43	22.4	18	2	AAR68679 Peptide C
24	43	22.4	18	2	AAR68679 HIV-1 env
25	43	22.4	18	2	AAR68679 HIV-1 V3

26	43	22.4	18	2	AAW99973	AAW99973 HIV-1 vac
27	43	22.4	18	2	AAW99973	AAW99973 HIV-1 vac
28	43	22.4	24	2	AAAR38170	AAAR38170 V3 loop p
29	43	22.4	33	2	AAAR68709	AAAR68709 p24H/PRI
30	43	22.4	33	2	AAAR68670	AAAR68670 p24E/V3 c
31	43	22.4	33	2	AAW25879	AAW25879 Chimaeric
32	43	22.4	33	2	AAW25840	AAW25840 Chimaeric
33	43	22.4	33	2	AAW67395	AAW67395 HIV-1 pep
34	43	22.4	33	2	AAW67356	AAW67356 HIV-1 pep
35	43	22.4	33	2	AAW98896	AAW98896 HIV-1 vac
36	43	22.4	33	2	AAW99964	AAW99964 HIV-1 vac
37	43	22.4	33	2	AAW39724	AAW39724 HIV-1 vac
38	43	22.4	33	2	AAW39762	AAW39762 HIV-1 vac
39	43	22.4	34	2	AAAR68674	AAAR68674 HIV-1 vac
40	43	22.4	34	2	AAW25844	AAW25844 Chimaeric
41	43	22.4	34	2	AAW67360	AAW67360 HIV-1 pep
42	43	22.4	34	2	AAW99968	AAW99968 HIV-1 vac
43	43	22.4	34	2	AAW39765	AAW39765 HIV-1 vac
44	43	22.4	35	2	AAAR21089	AAAR21089 PND EE15-
45	43	22.4	35	2	AAAR21090	AAAR21090 PND EE15-

ALIGNMENTS

RESULT 1		
AAR68713		
ID	AAR68713	standard; peptide; 33 AA.
XX	XX	
AC	AAR68713;	
XX	XX	
DT	16-OCT-2003	(revised)
DT	25-MAR-2003	(revised)
DT	07-SEP-1995	(first entry)
XX	XX	
DE	PRI/T5 chimera, CLTB-159.	
XX	XX	
KW	T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;	
XX	pol; vaccine; multimeric peptide; AIDS; 3D organisation.	
XX	XX	
OS	Human immunodeficiency virus 1.	
XX	XX	
Key	Location/Qualifiers	
FT	Peptide	1..18
FT	FT	/label= PRI
FT	FT	/note= "B cell epitope"
FT	FT	19..33
FT	FT	/label= T5
FT	FT	/note= "T cell epitope".


```
XX DE HIV-1 vaccine synthetic peptide SEQ ID NO:84.
XX KW HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN US5876731-A.
XX PD 02-MAR-1999.
XX PF 05-JUN-1995; 95US-00462507.
XX PR 09-JUN-1993; 93US-00073378.
XX PR 09-JUN-1994; 94US-00257528.
XX PA (CONN-) CONNAUGHT LAB LTD.
XX PI Chong P, Klein MH, Sia CDY;
XX WPI; 1999-189590/16.
XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
PT epitope linked to gp41 B-cell epitope.
XX Example 1; Col 63-64; 41pp; English.
XX CC The present invention describes a synthetic peptide comprising an amino
CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
CC its C terminus to an amino acid sequence containing a B-cell epitope of
CC an HIV gp41 protein and containing the amino acid sequence: X1LKDWX2;
CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
CC capable of eliciting an HIV-specific antiserum and recognizing the
CC sequence X1LKDWX2. The synthetic peptide is useful in vaccines against
CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
CC AAW98999 to AAW99989 represent synthetic peptides from the present
CC invention
XX SQ Sequence 33 AA;
XX Query Match 24.0%; Score 46; DB 2; Length 33;
XX Best Local Similarity 34.6%; Pred. No. 69;
XX Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
QY 8 TLPVGPGEFRTT-----LRVQNLG 27
DB 5 SIPIGPGRAFTTGYKYKWKIEPLG 30
RESULT 5
AAV39728
ID AAV39728 standard; peptide; 33 AA.
XX AC AAV39728;
XX DT 17-OCT-2003 (revised)
XX DT 26-NOV-1999 (first entry)
XX DE HIV1 chimeric peptide CLTB-159.
XX KW HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
XX infection; antibody; antiviral.
XX OS Human immunodeficiency virus 1.
XX PN US5951986-A.
XX PD 14-SEP-1999.
XX PF 06-JUN-1995; 95US-00467881.
XX
```

```
PR 09-JUN-1993; 93US-00073378.
XX 09-JUN-1994; 94US-00257528.
XX PA (CONN-) CONNAUGHT LAB LTD.
XX PI Klein MH, Chong P, Sia CDY;
XX WPI; 1999-550482/46.
XX Immunogenic composition containing synthetic fusion polypeptides
PT containing both the T and B cell epitopes of the human immunodeficiency
PT virus, useful antigens in producing vaccines.
XX Example 1; Col 25-26; 43pp; English.
XX This sequence represents a fragment of a HIV1 protein, and can be used in
CC the immunogenic composition of the invention. The composition comprises a
CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
CC carrier. Both the T cell and B cell epitopes are derived from HIV
CC proteins. The compositions are useful as vaccines against HIV infection.
CC The composition induces HIV-1-specific polyclonal antibodies that are
CC opsonising and antiviral. The peptide components may be selected to
CC induce a response against different viral isolates and in subjects who
CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX SQ Sequence 33 AA;
XX Query Match 24.0%; Score 46; DB 2; Length 33;
XX Best Local Similarity 34.6%; Pred. No. 69;
XX Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
QY 8 TLPVGPGEFRTT-----LRVQNLG 27
DB 5 SIPIGPGRAFTTGYKYKWKIEPLG 30
RESULT 6
AAV77763
ID AAV77763 standard; peptide; 35 AA.
XX AC AAV77763;
XX DT 16-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 08-SEP-1995 (first entry)
XX DE PRI/T5 chimera lysine branched peptide.
XX KW T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;
XX pol; vaccine; multimeric peptide; AIDS; 3D organisation.
XX OS Human immunodeficiency virus 1.
XX FH Key Location/Qualifiers
XX FT Peptide 1..18
XX FT /label= PRI
XX FT /note= "B cell epitope"
XX FT Peptide 19..33
XX FT /label= T5
XX FT /note= "T cell epitope"
XX FT Modified-site 34
XX FT /note= "Modified at the epsilon N by the sequence given
XX FT in AAR68713, which represents the same sequence as bases
XX FT 1-33 of this sequence"
XX FT Modified-site 35
XX FT /note= "Modified at the epsilon N with a Lys residue
XX FT which is substituted on the alpha and epsilon N with the
XX FT sequence given in AAR68713"
XX PN W09429339-A1.
XX
```


XX CC The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24b, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RF, Z6, 2054,
CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
CC Lys backbone. This sequence represents a chimaeric peptide comprising the
CC T-helper determinant core peptide T5 (AAW25881) with the HIV-1 strain MN
CC env protein V3 loop B-cell epitope PFI which corresponds to a peptide
CC generated from the consensus sequence of the New York and Amsterdam HIV-1
CC isolates. The B-cell epitope is linked to the C-terminus of the T-helper
CC peptide. (Updated on 25-MAR-2003 to correct PF field.)
XX CC
XX SQ Sequence 33 AA;

Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

QY 2 EVHPYG-----TLPVGPGEFKTT 20
::|||:::|||
Db 7 KIEPLGVAPNTRKSIPIGPGAFYTT 32

RESULT 9
AAW67398
ID AAW67398 standard; peptide; 33 AA.
XX AAW67398;
XX AC
XX AC
DT 25-JAN-1999 (first entry)
XX DE
XX DE HIV-1 peptide epitope CLTB-158.
XX KW Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
KW V3 loop.
XX OS Synthetic.
OS Human immunodeficiency virus 1.
XX OS
XX PN US5817754-A.
XX PD 06-OCT-1998.
XX PF 05-JUN-1995; 95US-00464329.
XX PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX PA
XX Chong P, Klein MH, Sia CDY;
PI WFI; 1998-556461/47.
DR
XX
XX Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
PT
XX Disclosure; Col 23-24; 40pp; English.
XX
XX The invention relates to a novel immunogenic composition for use in
CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
CC are generally designed based on the p24 core protein and the B-cell
CC epitopes from the V3 loop of the gp120 protein from various HIV-1
CC strains. This peptide corresponds to a fusion of the T5 epitope
CC (AAW67397) and the V3 loop B-cell epitope (AAW67365) which is a consensus
CC V3 loop peptide of the New York and Amsterdam HIV-1 isolates
XX

XX Identifying compounds that modify interaction of gp120 and co-receptors,
PT useful potentially for treating human immune deficiency virus infection,
PT also new peptides.
XX
XX
PS Disclosure; Fig 2; 68pp; German.
XX
XX This invention describes novel substances that modify the interaction
CC between the gp120 protein of human immunodeficiency virus (HIV), or its
CC fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
CC transmembrane receptors for HIV. The method comprises (a) immobilizing a
CC ligand for the co-receptor on a gold surface; (b) contacting the ligand
CC with suspended cells that express the co-receptor; and (c) determining
CC interaction by measuring the refractive index (RI) by plasmon resonance.
CC The procedure is repeated using cells that have been incubated with a
CC test compound, and this is identified if RI is lower for cells
CC preincubated with it. The ligand is a linear or cyclic (glyco)peptide
CC that includes the amino acid sequence of an HIV V3 loop (including
CC flanking Cys). The products of the invention have virucide and anti-HIV
CC (human immunodeficiency virus) activity and are useful for prevention
CC and/or treatment of HIV infection. This sequence represents an HIV-1 V3-
CC loop region described in the disclosure of the invention. (Updated on 29-
CC AUG-2003 to standardise OS field)
XX
SQ Sequence 35 AA;

Query Match 22.9%; Score 44; DB 5; Length 35;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 7; Indels 4; Gaps 1;
Qy 3 VHPYGT---LPVGGPPEFTTLRVQ 24
Db 2 IRPHNTVTDRIHIGGRSPHTTKIK 27

Search completed: April 6, 2005, 13:41:36
Job time : 169 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:44:50 ; Search time 139 Seconds
(without alignments)
83.596 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEVHPVGTLPVGPGEKTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 361004

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	23.2	35	US-10-424-599-185421	Sequence 185421,
2	43.5	22.7	28	US-10-443-622-133	Sequence 133, App
3	42	21.9	29	US-10-106-698-7462	Sequence 7462, Ap
4	42	21.9	35	US-10-424-599-238025	Sequence 238025,
5	40	20.8	23	US-10-125-869A-148	Sequence 148, App
6	40	20.8	23	US-10-462-262-372	Sequence 372, App
7	40	20.8	24	US-10-080-608A-71	Sequence 71, Appl
8	40	20.8	24	US-10-371-067-2	Sequence 2, Appl1
9	39	20.3	20	US-09-864-761-39770	Sequence 39770, A
10	39	20.3	21	US-09-864-761-46555	Sequence 46555, A
11	39	20.3	23	US-09-843-676-208	Sequence 208, App
12	39	20.3	23	US-09-438-486-208	Sequence 208, App
13	39	20.3	23	US-10-053-758-208	Sequence 208, App

14	39	20.3	23	14	US-10-054-295-208	Sequence 208, App
15	39	20.3	23	14	US-10-054-611-208	Sequence 208, App
16	39	20.3	23	15	US-10-325-810-327	Sequence 327, App
17	39	20.3	23	17	US-10-877-146-327	Sequence 327, App
18	39	20.3	24	10	US-09-798-889-167	Sequence 167, App
19	39	20.3	24	15	US-10-633-680-167	Sequence 167, App
20	39	20.3	35	10	US-09-759-947C-14	Sequence 14, Appl
21	38	19.8	15	9	US-09-810-310-27	Sequence 27, Appl
22	38	19.8	23	17	US-10-621-675-155	Sequence 155, App
23	38	19.8	24	10	US-09-933-767-472	Sequence 472, App
24	38	19.8	24	14	US-10-004-860-472	Sequence 472, App
25	38	19.8	24	14	US-10-023-282-472	Sequence 472, App
26	38	19.8	29	14	US-10-045-465-12	Sequence 12, Appl
27	38	19.8	33	14	US-10-272-339A-18	Sequence 18, Appl
28	38	19.8	33	14	US-10-272-339A-20	Sequence 20, Appl
29	37.5	19.5	30	15	US-10-057-475B-10828	Sequence 10828, A
30	37.5	19.5	30	15	US-10-154-884B-10828	Sequence 183, App
31	37	19.3	16	15	US-10-285-394-183	Sequence 104, App
32	37	19.3	16	15	US-10-601-837-104	Sequence 105, App
33	37	19.3	34	17	US-10-628-004-13	Sequence 13, Appl
34	36.5	19.0	27	11	US-09-833-245-1258	Sequence 1258, Ap
35	36.5	19.0	28	10	US-09-892-877-293	Sequence 293, App
36	36.5	19.0	28	10	US-09-948-783-305	Sequence 305, App
37	36.5	19.0	15	9	US-09-810-310-28	Sequence 28, Appl
38	36	18.8	15	14	US-10-320-175-7	Sequence 7, Appl1
39	36	18.8	15	17	US-10-701-682A-373	Sequence 373, App
40	36	18.8	17	10	US-09-964-201A-3	Sequence 3, Appl1
41	36	18.8	17	14	US-10-161-791-331	Sequence 331, App
42	36	18.8	17	16	US-10-681-389-3	Sequence 3, Appl1
43	36	18.8	17	16	US-10-681-388-3	Sequence 3, Appl1
44	36	18.8	22	10	US-09-932-613-167	Sequence 167, App
45	36	18.8				

ALIGNMENTS

RESULT 1

US-10-424-599-185421
; Sequence 185421, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185421
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13844C.1.pep
US-10-424-599-185421

Query Match 23.2%; Score 44.5; DB 15; Length 35;
Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 17 FKTLRVQNLG-CYVVS 32

Db 10 YNTARVDNLGDCYTLLA 26

RESULT 2

US-10-443-622-133
; Sequence 133, Application US/10443622
; Publication No. US20040024192A1

GENERAL INFORMATION:
 APPLICANT: Carter et al.
 TITLE OF INVENTION: 19 Human Secreted Proteins
 FILE REFERENCE: P2009P1
 CURRENT APPLICATION NUMBER: US/10/443,622
 PRIOR FILING DATE: 2003-05-23
 PRIOR APPLICATION NUMBER: PCT/US98/13608
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: 60/051,480
 PRIOR FILING DATE: 1997-07-01
 PRIOR APPLICATION NUMBER: 60/051,381
 PRIOR FILING DATE: 1997-07-01
 PRIOR APPLICATION NUMBER: 60/058,663
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: 60/058,598
 PRIOR FILING DATE: 1997-09-12
 NUMBER OF SEQ ID NOS: 156
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 133
 LENGTH: 28
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-443-622-133

Query Match 22.7%; Score 43.5; DB 15; Length 28;
 Best Local Similarity 42.1%; Pred. No. 1.1e+02;
 Matches 8; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Qy 4 HPYGTLPVGPQPEPKTTLR 22
 Db 7 HPVSS-PEGPGPQVRGARR 24

RESULT 3
 US-10-106-598-7462
 Sequence 7462, Application US/10106698
 Publication No. US20030109690A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 FILE REFERENCE: PA005P1
 CURRENT APPLICATION NUMBER: US/10/106,698
 PRIOR FILING DATE: 2002-03-27
 PRIOR APPLICATION NUMBER: PCT/US00/26524
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: US 60/157,137
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: US 60/163,280
 PRIOR FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO 7462
 LENGTH: 29
 TYPE: PRT
 ORGANISM: Homo sapiens
 NAME/KEY: MISC FEATURE
 LOCATION: (3)_FEATURE
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC FEATURE
 LOCATION: (6)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC FEATURE
 LOCATION: (7)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: MISC FEATURE
 LOCATION: (9)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-106-598-7462

Query Match 21.9%; Score 42; DB 14; Length 29;
 Best Local Similarity 56.2%; Pred. No. 1.9e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 4 HPYGTLPVGPQPEPKTTLR 22
 Db 11 HVEGKLVPPAGTGPPEF 26

RESULT 4
 US-10-424-599-238025
 Sequence 238025, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 238025
 LENGTH: 35
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_56963C.1.pap
 US-10-424-599-238025

Query Match 21.9%; Score 42; DB 15; Length 35;
 Best Local Similarity 70.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 PVGPGPEPKT 19
 Db 4 PAGPGPVFNT 13

RESULT 5
 US-10-125-869A-148
 Sequence 148, Application US/10125869A
 Publication No. US20030199671A1
 GENERAL INFORMATION:
 APPLICANT: Rondon, Isaac Jesus
 APPLICANT: Wu, Oi-Long
 APPLICANT: Ley, Arthur C.
 APPLICANT: Stochl, Mark
 APPLICANT: Ransohoff, Thomas C.
 APPLICANT: Potter, M. Daniel (deceased)
 TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
 FILE REFERENCE: 3421.1006-001
 CURRENT APPLICATION NUMBER: US/10/125,869A
 CURRENT FILING DATE: 2002-11-19
 PRIOR APPLICATION NUMBER: 60/284,534
 PRIOR FILING DATE: 2001-04-18
 NUMBER OF SEQ ID NOS: 200
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 148
 LENGTH: 23
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fc region binding polypeptide
 US-10-125-869A-148

Query Match 20.8%; Score 40; DB 14; Length 23;
 Best Local Similarity 43.8%; Pred. No. 2.8e+02;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YEHPYGTLPVGPPE 16
 Db 4 YWCNLMGVCPCANPGPE 19


```

; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NAF.P-003
; CURRENT APPLICATION NUMBER: US/10/371,067
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Fab59 complexed with a peptide mimic of the HIV-1 V3 loop
; OTHER INFORMATION: neutralization site.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-371-067-2

Query Match      20.8%; Score 40; DB 15; Length 24;
Best Local Similarity 44.4%; Pred. NO. 2.9e+02;
Matches      8; Conservative      3; Mismatches      5; Indels      2; Gaps      1;

QY      11 VGGPPEFKTTLRVQNLGC 28
          :|||  |||  :  :||
Db       9 IGGRXFYTKNI--IGC 24

RESULT 9
US-09-864-761-39770
; Sequence 39770, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-09-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

```

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 39770
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC005747.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;; OTHER INFORMATION: EST_HUMAN HIT: H87835.1, EVALUE 2.00e-06
US-09-864-761-39770

Query Match 20.3%; Score 39; DB 9; Length 20;
Best Local Similarity 58.3%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 HPYGTLPVGP 15
Db 1 HSWGTAKVGP 12

RESULT 10
US-09-864-761-46555
; Sequence 46555, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 46555
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009973.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
;; OTHER INFORMATION: EST_HUMAN HIT: AL121516.1, EVALUE 8.00e-07
US-09-864-761-46555

Query Match 20.3%; Score 39; DB 9; Length 21;
Best Local Similarity 57.9%; Pred. No. 3.4e+02;
Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 2;

Qy 2 EVHPYGTLPVGP 20
Db 6 DVH-RGTL---PGPNHKT 20

RESULT 11
US-09-843-676-208
; Sequence 208, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/843,676
;; FILING DATE: 26-Apr-2001
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US/08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US/08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US/08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 208:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-843-676-208

Query Match 20.3%; Score 39; DB 9; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPGTLPVGP 15
|||
Db 9 HPENLPQDP 20

RESULT 12
US-09-438-486-208
; Sequence 208, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002931US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 208:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-438-486-208

Query Match 20.3%; Score 39; DB 10; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPGTLPVGP 15
|||
Db 9 HPENLPQDP 20

RESULT 13
US-10-053-758-208
; Sequence 208, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/846,017

; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-053-758-208

Query Match 20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPYGTLPVGGP 15
||| |||
Db 9 HPRENLPQDPGP 20

RESULT 14
US-10-054-295-208
; Sequence 208, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-054-295-208
Query Match 20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 HPYGTLPVGGP 15
||| |||
Db 9 HPRENLPQDPGP 20
RESULT 15
US-10-054-611-208
; Sequence 208, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid

```

; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-054-611-208

Query Match      20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      4 HPYGTLPVGP GP 15
      |||||
Db      9 HPRENLPQDP GP 20

```

Search completed: April 6, 2005, 13:57:33
Job time : 140 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:32:19 ; Search time 42 Seconds
(without alignments)
62.208 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986
Perfect score: 192
Sequence: 1 YEHVPYGLVPGPGPEKFTLRVQNLCYVVSGLI 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 250370

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	24.0	33	1	US-08-257-528B-84
2	46	24.0	33	1	US-08-460-602A-84
3	46	24.0	33	1	US-08-463-966A-84
4	46	24.0	33	1	US-08-465-217A-84
5	46	24.0	33	2	US-08-464-329A-84
6	46	24.0	33	2	US-08-462-507A-84
7	46	24.0	33	2	US-08-467-881A-84
8	46	24.0	34	3	US-09-141-833-11
9	45.5	23.7	33	1	US-08-257-528B-83
10	45.5	23.7	33	1	US-08-460-602A-83
11	45.5	23.7	33	1	US-08-463-966A-83
12	45.5	23.7	33	1	US-08-465-217A-83
13	45.5	23.7	33	2	US-08-464-329A-83
14	45.5	23.7	33	2	US-08-462-507A-83
15	45.5	23.7	33	2	US-08-467-881A-83
16	45	23.4	35	3	US-08-513-968-13
17	43.5	22.7	33	1	US-08-257-528B-81
18	43.5	22.7	33	1	US-08-460-602A-81
19	43.5	22.7	33	1	US-08-463-966A-81
20	43.5	22.7	33	1	US-08-465-217A-81
21	43.5	22.7	33	2	US-08-464-329A-81
22	43.5	22.7	33	2	US-08-462-507A-81
23	43.5	22.7	33	2	US-08-467-881A-81
24	43	22.4	18	1	US-08-257-528B-50
25	43	22.4	18	1	US-08-460-602A-50
26	43	22.4	18	1	US-08-463-966A-50
27	43	22.4	18	1	US-08-465-217A-50

28	43	22.4	18	2	US-08-464-329A-50	Sequence 50, Appl
29	43	22.4	18	2	US-08-462-507A-50	Sequence 50, Appl
30	43	22.4	18	2	US-08-467-881A-50	Sequence 50, Appl
31	43	22.4	23	3	US-08-513-968-71	Sequence 71, Appl
32	43	22.4	23	3	US-08-513-968-72	Sequence 72, Appl
33	43	22.4	33	1	US-08-257-528B-41	Sequence 41, Appl
34	43	22.4	33	1	US-08-257-528B-80	Sequence 80, Appl
35	43	22.4	33	1	US-08-460-602A-41	Sequence 41, Appl
36	43	22.4	33	1	US-08-460-602A-80	Sequence 80, Appl
37	43	22.4	33	1	US-08-463-966A-41	Sequence 41, Appl
38	43	22.4	33	1	US-08-463-966A-80	Sequence 80, Appl
39	43	22.4	33	1	US-08-465-217A-41	Sequence 41, Appl
40	43	22.4	33	1	US-08-465-217A-80	Sequence 80, Appl
41	43	22.4	33	2	US-08-464-329A-41	Sequence 41, Appl
42	43	22.4	33	2	US-08-464-329A-80	Sequence 80, Appl
43	43	22.4	33	2	US-08-462-507A-41	Sequence 41, Appl
44	43	22.4	33	2	US-08-462-507A-80	Sequence 80, Appl
45	43	22.4	33	2	US-08-467-881A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-08-257-528B-84
; Sequence 84, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-257-528B-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
Qy 8 TLPVGPGEPEKFT-----LRVQNIG 27
Db 5 SIPIGPGRAFTYTGKVKVIEPLG 30

```
RESULT 2
US-08-460-602A-84
; Sequence 84, Application US/08460602A
; Patent No. 5795969
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460.602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-460-602A-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Qy 8 TLPVGPPEPKTT-----LRVQNLG 27
Db 5 SIPIGPGAFYTTGYKYKVKVIEPLG 30

RESULT 3
US-08-463-966A-84
; Sequence 84, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
```

```
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,966A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-966A-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Qy 8 TLPVGPPEPKTT-----LRVQNLG 27
Db 5 SIPIGPGAFYTTGYKYKVKVIEPLG 30

RESULT 4
US-08-465-217A-84
; Sequence 84, Application US/08465217A
; Patent No. 5800822
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,217A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
```



```
; Sequence 84, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jbb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-467-881A-84
;
; Query Match 24.0%; Score 46; DB 2; Length 33;
; Best Local Similarity 34.6%; Pred. No. 8.7;
; Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
;
; Qy 8 TLPVGGPPEFKTT-----LRVQNIG 27
; Db 5 SIPIGPGRAFTYTGYYKVKVIEPLG 30
;
; RESULT 8
; US-09-141-833-11
; Sequence 11, Application US/09141833
; Patent No. 6168784
; GENERAL INFORMATION:
; APPLICANT: OFFORD, ROBIN E
; APPLICANT: THOMPSON, DARREN
; APPLICANT: WILKEN, JILL
; TITLE OF INVENTION: N-TERMINAL MODIFICATIONS OF RANTES AND METHODS OF USE
; FILE REFERENCE: GRFN-026/03US
; CURRENT APPLICATION NUMBER: US/09141,833
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: 60/056,292
; EARLIER FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 60/077,874
; EARLIER FILING DATE: 1998-03-13
; EARLIER APPLICATION NUMBER: 60/090,834
;
; Sequence 84, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jbb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-467-881A-84
;
; Query Match 24.0%; Score 46; DB 2; Length 33;
; Best Local Similarity 34.6%; Pred. No. 8.7;
; Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
;
; Qy 8 TLPVGGPPEFKTT-----LRVQNIG 27
; Db 5 SIPIGPGRAFTYTGYYKVKVIEPLG 30
;
; RESULT 8
; US-09-141-833-11
; Sequence 11, Application US/09141833
; Patent No. 6168784
; GENERAL INFORMATION:
; APPLICANT: OFFORD, ROBIN E
; APPLICANT: THOMPSON, DARREN
; APPLICANT: WILKEN, JILL
; TITLE OF INVENTION: N-TERMINAL MODIFICATIONS OF RANTES AND METHODS OF USE
; FILE REFERENCE: GRFN-026/03US
; CURRENT APPLICATION NUMBER: US/09141,833
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: 60/056,292
; EARLIER FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 60/077,874
; EARLIER FILING DATE: 1998-03-13
; EARLIER APPLICATION NUMBER: 60/090,834
;
; Sequence 84, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-141-833-11
;
; Query Match 24.0%; Score 46; DB 3; Length 34;
; Best Local Similarity 47.4%; Pred. No. 9;
; Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
;
; Qy 8 TLPVGGPPEFKTTLRVQNL 26
; Db 11 SISIGPGRAFTTQIVGNL 29
;
; RESULT 9
; US-08-257-528B-83
; Sequence 83, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jbb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-257-528B-83
;
; Query Match 23.7%; Score 45.5; DB 1; Length 33;
; Best Local Similarity 34.6%; Pred. No. 10;
; Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;
;
; Qy 2 EVHPYGV-----TLPVGGPPEFKTT 20
; Db 7 KIEPLGVAPNTRKSIPIGPGRAFTT 32
;
; RESULT 10
; US-08-460-602A-83
; Sequence 83, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
```

;; APPLICANT: SIA, Charles D.Y.
;; APPLICANT: CHONG, Pele
;; APPLICANT: KLEIN, Michel H.
;; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
;; NUMBER OF SEQUENCES: 101
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/460,602A
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/073,378
;; FILING DATE: 09-JUN-1994
;; CLASSIFICATION: 424
;; NAME: STEWART, MICHAEL I.
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 83:
;; LENGTH: 33 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-460-602A-83

Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 11
US-08-463-966A-83
; Sequence 83, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/463,966A
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/257,528
;; FILING DATE: 09-JUN-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/073,378
;; FILING DATE: 09-JUN-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEWART, MICHAEL I.
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 83:
;; LENGTH: 33 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-463-966A-83

Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 12
US-08-465-217A-83
; Sequence 83, Application US/08465217A
; Patent No. 5800822
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,217A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

```
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-465-217A-83
Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEPEKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 13
US-08-464-329A-83
; Sequence 83, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,329A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-464-329A-83
Query Match 23.7%; Score 45.5; DB 2; Length 33;
```

```
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-462-507A-83
Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEPEKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 14
US-08-462-507A-83
; Sequence 83, Application US/08462507A
; Patent No. 5876731
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,507A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-462-507A-83
Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEPEKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 15
US-08-467-881A-83
; Sequence 83, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
```

APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-83

Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPVG-----TLPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGGRFYTT 32

Search completed: April 6, 2005, 13:45:31
Job time : 43 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:42:11 ; Search time 43 Seconds
(without alignments)
49.227 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFPAHKKIPPEEKREKLEQ 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4267

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	35.1	19	2 A49725	valine-tRNA ligase
2	30	26.3	20	2 I53671	neurofilament heav
3	29	25.4	17	2 S10786	enamelin, 26K - bo
4	29	25.4	20	2 S43627	cytochrome-c oxida
5	28	24.6	10	2 S65385	cytochrome-c oxida
6	27	23.7	8	2 I64832	Ca2+-transporting
7	27	23.7	15	2 PA0041	plastoquinol-plast
8	27	23.7	16	2 S13898	alkaline phosphata
9	27	23.7	17	2 G83975	hypothetical prote
10	27	23.7	18	2 A81220	epsilon receptor m
11	27	23.7	20	2 S11416	ribosomal protein
12	26	22.8	15	2 S36891	ribosomal protein
13	26	22.8	18	2 E33178	78K heat shock pro
14	26	22.8	21	2 PC7043	ubiquitin carboxyl
15	26	22.8	22	2 F33084	ribosomal protein
16	26	22.8	22	2 PC4388	sulfite reductase
17	25	21.9	16	2 JH0517	insulin-like growt
18	25	21.9	16	2 A35552	caldesmon - turkey
19	25	21.9	18	2 S39845	2-aminobenzoate-Co
20	25	21.9	20	2 D49164	chromogranin-B - r
21	25	21.9	20	2 S06149	photosystem I chai
22	25	21.9	20	2 S77983	cytochrome-c oxida
23	25	21.9	22	2 PX0078	alanine dehydrogen
24	24.5	21.5	21	2 S00189	motilin - dog (ten
25	24	21.1	14	2 S65392	cytochrome-c oxida
26	24	21.1	18	2 B44995	alkanal monooxygen
27	24	21.1	19	2 A37968	neural surface pro
28	24	21.1	22	2 H86433	protein ti7H7.9 [i
29	23.5	20.6	19	2 S02808	nucleolin - bovine

30	23	20.2	14	2 A49018	myosin heavy chain
31	23	20.2	15	2 C37765	hypothetical prote
32	23	20.2	18	2 I40062	shikimate 5-dehydr
33	23	20.2	19	2 S69166	ferredoxin b - Jap
34	23	20.2	20	2 JP0070	ribosomal protein
35	23	20.2	20	2 A31516	lectin, galactose/
36	23	20.2	20	2 S06150	photosystem I chai
37	23	20.2	20	2 S19618	globin - polychaet
38	23	20.2	21	2 S78416	ribosomal protein
39	23	20.2	22	2 JP0071	ribosomal protein
40	23	20.2	22	2 C64330	ribosomal protein
41	23	20.2	22	2 S78007	fucosyltransferase
42	23	20.2	22	2 S48196	fucosyltransferase
43	22.5	19.7	20	2 A05310	apolipoprotein E -
44	22	19.3	10	2 S43625	cytochrome-c oxida
45	22	19.3	12	2 S16335	beta-conglycinin a

ALIGNMENTS

RESULT 1

A49725 valine-tRNA ligase (EC 6.1.1.9) - rabbit (fragment)

N;Alternate names: valyl-tRNA synthetase

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Jun-2002

C;Accession: A49725

R;Bec. G.; Kerjan, P.; Waller, J.P.

J. Biol. Chem. 269, 2086-2092, 1994

A;Title: Reconstitution in Vitro of the valyl-tRNA synthetase-elongation factor (EF) 1be

Ita subunit in complex formation.

A;Reference number: A49725; MUID:94124563; PMID:8294461

A;Accession: A49725

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <BEC>

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 35.1%; Score 40; DB 2; Length 19;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 9 KIPEEKREKLEQ 22

Db 2 QLPXEAKKNEKLEK 15

RESULT 2

I53671 neurofilament heavy subunit - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I53671

R;Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.

Gene 132, 297-300, 1993

A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament hea

A;Reference number: I53671; MUID:94040777; PMID:8224877

A;Accession: I53671

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-20 <RES>

A;Cross-references: UNIPROT:Q16070; GB:S66488; NID:g452861; PIDN:AAB28609.1; PID:g452862

C;Genetics:

A;Gene: GDB:NEFH

A;Cross-references: GDB:I20225; OMIM:162230

A;Map position: 22q12.1-22q13.1

Query Match

Best Local Similarity 26.3%; Score 30; DB 2; Length 20;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 9 KIPEEKREKLE 21

```
Db      |||: |||
        6 KSPEKAKSPEKEE 18

RESULT 3
SI0786
enamelin, 26K - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: SI0786
R:Strawich, B.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu
A:Reference number: SI0780; MUID:90336641; PMID:2379503
A:Accession: SI0786
A:Molecule type: Protein
A:Residues: 1-17 <STR>
A:Cross-references: UNIPROT:Q7M2M6
C:Keywords: enamel; phosphoprotein

Query Match      25.4%; Score 29; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 HKKIP 11
        |||||
        10 HKKIP 14

RESULT 4
S43627
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
C:Species: Salmo g. (trout)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
C:Accession: S43627
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochr
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43627
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <FRE>
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      8 KKIPEEKREKLEQ 22
        |||: |||
        4 KGIPDSEQATGLSE 18

RESULT 5
S65385
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C:Accession: S65385
R:Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A:Reference number: S65372; MUID:93324529; PMID:7601105
A:Accession: S65385
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SCH>
C:Keywords: oxidoreductase

Query Match      24.6%; Score 28; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      9 KIPEEK 15
        |||: |||
        4 KVPEKQK 10
```

RESULT 6

```
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I64832
R;Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase 1
A:Reference number: I51892
A:Accession: I64832
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646
C:Genetics:
A:Gene: SERCALB
C:Keywords: hydrolase
```

```
Query Match      23.7%; Score 27; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      11 PEEKRE 17
        ||: |||
        2 PEDERRK 8
```

RESULT 7

```
PA0041
plastoquinol-plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PA0041
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional:
A:Reference number: PA0001
A:Accession: PA0041
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Cross-references: UNIPROT:Q92R03; UNIPROT:Q94E14; UNIPROT:Q9FYB6
A:Experimental source: leaf
C:Keywords: oxidoreductase
```

```
Query Match      23.7%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      9 KIPEEKR 16
        :||: |||
        8 RVFDMERK 15
```

RESULT 8

```
SI3898
alkaline phosphatase (EC 3.1.3.1) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: SI3898
R;Fujimori-Arai, Y.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.
Arch. Biochem. Biophys. 284, 320-325, 1991
A:Title: Purification and partial characterization of intestinal-like alkaline phosphatase
A:Reference number: SI3898; MUID:91112827; PMID:1989515
A:Accession: SI3898
A:Status: preliminary
A:Molecule type: protein
```


A;Residues: 1-16 <FUJ>
A;Cross-references: UNIPROT:Q7M2K8
C;Keywords: phosphoric monoester hydrolase

Query Match 23.7%; Score 27; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IPEEEK 15
| | | | |
Db 2 IPEEEE 7

RESULT 9

G83975
Hypothetical protein BH2607 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83975
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83975
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <STO>
A;Cross-references: UNIPROT:Q9K9N8; GB:AP001516; GB:BA000004; NID:gi10175192; PIDN:BA063
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2607

Query Match 23.7%; Score 27; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEKLE 21
| | | | |
Db 2 KEIPTKMKTEKDE 15

RESULT 10

A61220
epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A61220
R;Matsushita, S.; Katz, D.H.
Cell. Immunol. 137, 252-259, 1991
A;Title: The murine epsilon receptor modulating protein: a novel serine protease which m
A;Reference number: A61220; MUID:91356570; PMID:1679381
A;Accession: A61220
A;Molecule type: protein
A;Residues: 1-18 <MAT>
A;Cross-references: UNIPROT:Q7M060
C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C;Keywords: hydrolase; serine proteinase

Query Match 23.7%; Score 27; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEK 19
| | | | |
Db 2 KPAPKEEKKK 13

RESULT 11

S11416
ribosomal protein L6, cytosolic [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C;Accession: S11416

R;Wittmann-Liebold, B.; Geissler, A.W.; Lin, A.; Wool, I.G.
J. Supramol. Struct. 12, 425-433, 1979
A;Title: Sequence of the amino-terminal region of rat liver ribosomal proteins S4, S6, S8
A;Reference number: S11413; MUID:80252792; PMID:398910
A;Accession: S11416

A;Molecule type: protein
A;Residues: 1-20 <WIT>
A;Note: the protein is designated as ribosomal protein L6
C;Keywords: protein biosynthesis; ribosome

Query Match 23.7%; Score 27; DB 2; Length 20;
Best Local Similarity 35.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AHKKIPEEEKREEK 19
| | | | |
Db 1 AGEKAEKPKKEQK 14

RESULT 12

S36891
ribosomal protein - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S36891
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac.
A;Reference number: S36887; MUID:94009653; PMID:8405418
A;Accession: S36891
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <OHA>
A;Cross-references: UNIPROT:Q9R545

Query Match 22.8%; Score 26; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEK 19
| | | | |
Db 3 KNVPANRRKAK 14

RESULT 13

E33178
78K heat shock protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 23-Mar-1993
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro.
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: E33178
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <WAR>

Query Match 22.8%; Score 26; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEEKREE 18
| | | | |
Db 2 EEDKKED 8

RESULT 14

PC7043
ubiquitin carboxyl-terminal hydrolase (EC 3.1.1.-) homolog - yeast (Pichia anomala) (fra
N;Alternate names: ALX1 protein
C;Species: Pichia anomala, Candida pelliculosa

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
 C;Accession: PC7043
 R/Sakajo, S.; Minagawa, N.; Yoshimoto, A.
 Biosci. Biotechnol. Biochem. 63, 1889-1894, 1999
 A;Title: Structure and regulatory expression of a single copy alternative oxidase gene
 A;Reference number: JC7145; MUID:20101471; PMID:10635554
 A;Accession: PC7043
 A;Molecule type: DNA
 A;Residues: 1-21 <SAK>
 A;Cross-references: UNIPROT:Q9P987; DDBJ:AB026726
 C;Genetics:
 A;Gene: aix1
 C;Keywords: hydrolase

Query Match 22.8%; Score 26; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 EKREKLEQ 22
 |::|::|
 Db 12 EDKREGKEE 21

RESULT 15
 F33084
 ribosomal protein L18 - Haloflex mediterranei (fragment)
 N;Alternate names: ribosomal protein HL13
 C;Species: Haloflex mediterranei
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: F33084
 R;McDougall, J.
 submitted to the Protein Sequence Database, June 1990
 A;Reference number: A33084
 A;Accession: F33084
 A;Molecule type: Protein
 A;Residues: 1-22 <MCD>
 A;Cross-references: UNIPROT:P50561
 A;Experimental source: strain DSM 1411
 C;Superfamily: rat ribosomal protein L5
 C;Keywords: protein biosynthesis; ribosome

Query Match 22.8%; Score 26; DB 2; Length 22;
 Best Local Similarity 30.8%; Pred. No. 2.7e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 9 KIPREKLE 21
 |::|::|
 Db 7 KVPMPRRREVTD 19

Search completed: April 6, 2005, 14:59:35
 Job time : 45 secs


```

RX MEDLINE=92319557; PubMed=1352398;
RA Hogg A., Onadim Z., Baird P.N., Cowell J.K.;
RT "Detection of heterozygous mutations in the RB1 gene in retinoblastoma
RT patients using single-strand conformation polymorphism analysis and
RT polymerae chain reaction sequencing.";
RL Oncogene 7:1445-1451(1992).
DR EMBL; AY243567; AAC62758.1; -.
DR EMBL; L41913; AAA65748.1; -.
FT NON TER 1
FT NON TER 16
SQ SEQUENCE 16 AA; 1871 MW; 3A6A9791FD68E1E9 CRC64;

Query Match 28.1%; Score 32; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPKREKLEQ 22
Db 1 KHLFGSKFQQLAE 15

RESULT 3
Q91983 PRELIMINARY; PRT; 19 AA.
AC Q91983;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC (19 AA) (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88040428; PubMed=3671071;
RA McCarthy J.G., Heywood S.M.;
RT "A long polypyrimidine/polypurine tract induces an altered DNA
RT conformation on the 3' coding region of the adjacent myosin heavy
RT chain gene.";
RL Nucleic Acids Res. 15:8069-8085(1987).
FT NON TER 1
SQ SEQUENCE 19 AA; 2387 MW; 2DD5C6816CD4D6EC CRC64;

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 70.0%; Pred. No. 2.8e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FAHKKIPPEE 14
Db 10 FHSKKIEEEE 19

RESULT 4
Q789B3 PRELIMINARY; PRT; 19 AA.
AC Q789B3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89210285; PubMed=2707122;
RA Lagrutta A.A., McCarthy J.G., Scherzinger C.A., Heywood S.M.;
RT "Identification and developmental expression of a novel embryonic
RT myosin heavy-chain gene in chicken.";
RL DNA 8:39-50(1989).
DR EMBL; M24691; AAA48950.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 19 AA; 2387 MW; 2DD5C6816CD4D6EC CRC64;

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 70.0%; Pred. No. 2.8e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FAHKKIPPEE 14
Db 10 FHSKKIEEEE 19

RESULT 5
Q9380 PRELIMINARY; PRT; 13 AA.
AC Q9380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IFA binding protein (sp10) (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DOK; TISSUE=Curd surface;
RA Wallis G.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97678; CAA66268.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1413 MW; D1D4EA3926B42772 CRC64;

Query Match 26.3%; Score 30; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AHKKIPPEE 13
Db 2 AEKKVPKE 9

RESULT 6
Q16070 PRELIMINARY; PRT; 20 AA.
AC Q16070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neurofilament heavy subunit (Fragment).
GN Name=NEFH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94040777; PubMed=8224877; DOI=10.1016/0378-1119(93)90211-K;
RA Figlewicz D.A., Rouleau G.A., Krizus A., Julien J.P.;
RT "Polymorphism in the multi-phosphorylation domain of the human
RT neurofilament heavy-subunit-encoding gene.";
RL Gene 132:297-300(1993).
DR EMBL; S66488; AAB28609.1; -.
DR PIR; I53671; I53671.

```

```

FT NON TER 20 20
SQ SEQUENCE 20 AA; 2198 MW; E9A0975B41FD8082 CRC64;

Query Match 26.3%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 4.1e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 9 KIPEEKKEEKKLE 21
Db 6 KSPKAKSPKEKE 18

RESULT 7
Q9RSU3 ID Q9RSU3 PRELIMINARY; PRT; 22 AA.
AC Q9RSU3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA LIGASE=E2 (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OX NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=91358327; PubMed=1885526;
RA Alteschmidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp.";
RL J. Bacteriol. 173:5494-5501(1991).
FT NON TER 1 1
FT NON TER 22 22
SQ SEQUENCE 22 AA; 2526 MW; 5D37FA76363F8792 CRC64;

Query Match 26.3%; Score 30; DB 2; Length 22;
Best Local Similarity 37.5%; Pred. No. 4.5e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 5 FAHKKIPPEEKKEEKL 20
Db 7 FARDXPPEEQTESL 22

RESULT 8
Q9TRY7 ID Q9TRY7 PRELIMINARY; PRT; 20 AA.
AC Q9TRY7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-5, IGFBP-5 (Fragment).
OS Sus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.
RX MEDLINE=92049376; PubMed=1719383;
RA Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2185 MW; F77C34A8FA94EF9 CRC64;

Query Match 25.9%; Score 29.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 LGFFAHKKIPPEEK 15

```

```

Db 1 LGSFVHXE-PADEX 13

RESULT 9
Q7M2M6 ID Q7M2M6 PRELIMINARY; PRT; 17 AA.
AC Q7M2M6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Enamelin, 26K (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=90336641; PubMed=2379503;
RA Strawich E., Glimcher M.J.;
RT "Tooth 'enamelins' identified mainly as serum proteins. Major
RT 'enamelin' is albumin.";
RL Eur. J. Biochem. 191:47-56(1990).
DR PIR: S10786; S10786.
FT NON TER 1 1
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2137 MW; FFA54E4CEE066720 CRC64;

Query Match 25.4%; Score 29; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 HKKIP 11
Db 10 HKKIP 14

RESULT 10
COXF ONCMY ID COXF ONCMY STANDARD; PRT; 20 AA.
AC P80329;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome c oxidase polypeptide Vb-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and Vifa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Vb family.
DR InterPro; IPR002124; COX5B.
DR PROSITE; PS00848; COX5B; PARTIAL.
KW Direct protein sequencing; Inner membrane; Mitochondrion;
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2184 MW; 6A8E00CEB33E92BD7 CRC64;

```

Query Match 25.4%; Score 29; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.6e+03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 8 KKIPEEKREKLEK 22
|||:|:|:
DB 4 KGIPTDEQATGLEE 18

RESULT 11

BNCB_BENHI STANDARD; PRT; 14 AA.
AC P83961;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Beta benincasin (Fragment).
OS Benincasa hispida (wax gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Benincasa.
OX NCBI_TaxID=102211;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=Dong-gua; TISSUE=Seed;
RX PubMed=12576080; DOI=10.1016/S0196-9781(02)00271-1;
RA Ng T.B., Parkash A., Tso W.W.;
RT "Purification and characterization of alpha- and beta-benincasins.
RT arginine/glutamate-rich peptides with translation-inhibiting activity
RT from wax gourd seeds.";
RL Peptides 24:11-16(2003).
CC -I- FUNCTION: Inhibits cell-free translation in rabbit reticulocyte
CC lysate system.
CC -I- MISCELLANEOUS: IC(50) of 320 pM in rabbit reticulocyte.
KW Direct protein sequencing.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 2056 MW; D442D6DF5B079106 CRC64;

Query Match 24.6%; Score 28; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEKREK 19
|||:|:|:
DB 6 EQERRQER 13

RESULT 12

Q9UCQ3 PRELIMINARY; PRT; 22 AA.
AC Q9UCQ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE KU antigen 73 kDa protein fraction 31 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165807; PubMed=1537839;
RA Wedrychowski A., Henzel W., Huston L., Paslidis N., Ellerson D.,
RA McRae M., Seong D., Howard O.M., Deisseroth A.;
RT "Identification of proteins binding to interferon-inducible
RT transcriptional enhancers in hematopoietic cells.";
RL J. Biol. Chem. 267:4533-4540(1992).
DR GO; GO:0003677; F:DNA binding; NAS.
FT NON_TER 1 1
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2488 MW; 24B2B59F08AF2996 CRC64;

Query Match 24.6%; Score 28; DB 2; Length 22;

Best Local Similarity 66.7%; Pred. No. 8.4e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 EEKREKLE 21
|||:|:|:
DB 8 EEDEENLE 16

RESULT 13

Q9RSZ5 PRELIMINARY; PRT; 15 AA.
AC Q9RSZ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Streptolysin O (Fragment).
OC Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273535; PubMed=8500915;
RA Gerlach D., Kohler W., Gunther S., Mann K.;
RT "Purification and characterization of streptolysin O secreted by
RT Streptococcus equisimilis (group C).";
RL Infect. Immun. 61:2727-2731(1993).
SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 24.1%; Score 27.5; DB 2; Length 15;
Best Local Similarity 46.7%; Pred. No. 6.7e+03;
Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 6 AHKKIP-EEKREK 19
|||:|:|:|:
DB 1 APKEMPLESAREEK 15

RESULT 14

Q78ED1 PRELIMINARY; PRT; 8 AA.
AC Q78ED1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium transporting ATPase (Fragment).
GN Name=SERCALB;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD; TISSUE=Skeletal muscle;
RX MEDLINE=93191041; PubMed=8447366;
RA Wu K.-D., Lytton J.;
RT "Molecular cloning and quantification of mRNA and protein encoding
RT Ca2+-ATPase isoforms in rat muscles.";
RL Am. J. Physiol. 264:333-341(1993).
DR EMBL; M99223; AAA40992.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1044 MW; D724140B1AAB076A CRC64;

Query Match 23.7%; Score 27; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 PEEKRE 17
|||:|:|:
DB 2 PEDERRK 8

RESULT 15

Q6LDS7
ID Q6LDS7 PRELIMINARY; PRT; 9 AA.
AC Q6LDS7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DS Ca2+ ATPase (Fragment);
OS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast twitch muscle;
RX MEDLINE=88169602; PubMed=2965149;
RA Korczak B., Zarain-Herzberg A., Brandl C.J., Ingles C.J., Green N.M.,
RA MacLennan D.H.;
RT "Structure of the rabbit fast-twitch skeletal muscle Ca2+-ATPase
gene";
RL J. Biol. Chem. 263:4813-4819(1988).
DR EMBL; M20532; AAA31174.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1173 MW; 8235140B1AAB076A CRC64;

Query Match 23.7%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PEEKRE 17
Db 3 PEDERRK 9

Search completed: April 6, 2005, 14:55:45
Job time : 176 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:41:35 ; Search time 174 Seconds
(without alignments)
48.901 Million cell updates/sec

Title: US-09-647-544-7
Perfect score: 114
Sequence: 1 KLGFPAHKIPBEKREKLEQ 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 740715

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	22	3	AAY32244 Human int
2	44	38.6	19	6	ABP56388 Polyamion
3	44	38.6	20	4	AAB59156 Alpha IIB
4	43	37.7	20	2	AAR8078 Integrin
5	43	37.7	20	4	AAB59147 Alpha IIB
6	42	36.8	19	2	AAW48683 Amino aci
7	39	34.2	7	8	ADA27160 Human int
8	39	34.2	7	8	ADI39445 Integrin
9	39	34.2	15	6	ABP94377 HLA prote
10	39	34.2	15	6	ABP93904 HLA prote
11	39	34.2	15	6	ABP94921 HLA prote
12	39	34.2	15	6	ABP95230 HLA prote
13	39	34.2	20	5	AAU85587 Lung tumo
14	39	34.2	20	6	ABU69559 Human lun
15	39	34.2	20	6	ABU66462 Lung canc
16	39	34.2	20	7	ADH47374 Human lun
17	39	34.2	20	8	ADJ21293 Human lun
18	38	33.3	22	4	AAM16576 Peptide #
19	38	33.3	22	4	ABM20986 Protein #
20	38	33.3	22	4	AAM68751 Human bon
21	37	32.5	15	6	ABP95115 HLA prote
22	37	32.5	15	6	ABP94987 HLA prote
23	37	32.5	15	6	ABP93956 HLA prote
24	37	32.5	15	6	ABP93368 HLA prote
25	37	32.5	15	6	ABP94457 HLA prote

26	37	32.5	15	6	ABP95241 HLA prote
27	37	32.5	15	6	ABP94244 HLA prote
28	37	32.5	15	6	ABP94458 HLA prote
29	37	32.5	15	6	ABP93790 HLA prote
30	37	32.5	15	6	ABP94825 HLA prote
31	37	32.5	15	8	ADI32231 Cosmectic
32	37	32.5	15	8	ADO76553 Human 213
33	37	32.5	20	5	AAU85588 Lung tumo
34	37	32.5	20	6	ABU69560 Human lun
35	37	32.5	20	6	ABU66463 Lung canc
36	37	32.5	20	7	ADH47375 Human lun
37	37	32.5	20	8	ADJ21294 Human lun
38	36	31.6	13	4	AAB99530 Human Hsp
39	36	31.6	13	5	ABB74746 Transcrip
40	36	31.6	14	4	AAB59149 Alpha IIB
41	36	31.6	16	4	AAB99524 Human Hsp
42	36	31.6	16	4	AAB59148 Alpha IIB
43	36	31.6	17	4	AAB99533 Hsp70B' i
44	36	31.6	18	3	AAV52610 v-myb enc
45	36	31.6	19	2	AAW14811 myb oncog

ALIGNMENTS

RESULT 1

AAV32244	
ID	AAV32244 standard; peptide; 22 AA.
XX	
AC	AAV32244;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Human integrin subunit alpha-10 cytoplasmic domain peptide.
XX	
KW	Integrin alpha-10; ISa10; human; trauma; rheumatoid arthritis;
KW	osteoarthritis; osteoarthritis; cancer; atherosclerosis; inflammation;
KW	therapy; cartilage; chondrocyte; osteoblast; fibroblast; vaccine; marker.
XX	
OS	Homo sapiens.
XX	
PN	WO9951639-A1.
XX	
PD	14-OCT-1999.
XX	
PF	31-MAR-1999; 99WO-SE000544.
XX	
PR	02-APR-1998; 98SE-00001164.
PR	28-JAN-1999; 99SE-00000319.
XX	
PA	(ACTI-) ACTIVE BIOTECH AB.
XX	
PI	Lundgren-Akerlund E;
XX	
DR	WPI; 2000-052639/04.
XX	

New isolated integrin subunit alpha-10, used as a marker or target molecule for cells during development, regeneration and pathological conditions, e.g. arthritis, osteoarthritis, cancer, atherosclerosis or inflammation.

Claim 21; Page 53; 90pp; English.

This sequence represents a fragment of novel human chondrocyte integrin subunit alpha-10 (ISa10, see AAV32242), corresponding to the C-terminal cytoplasmic domain of the protein. The invention relates to a recombinant or isolated integrin heterodimer comprising the alpha10 subunit in association with subunit beta (especially beta-1). The integrin heterodimer, or the subunit alpha-10, or a fragment of it such as the present sequence, can be used as a marker or target of all types of cells, e.g. of chondrocytes, osteoblasts and fibroblasts. They can also be used: for treating pathological conditions involving ISa10, such as damage to cartilage, trauma, rheumatoid arthritis or osteoarthritis; for

CC detecting the formation of cartilage during embryonal development,
 CC physiological or therapeutic repair of cartilage, or detecting
 CC regeneration of cartilage or chondrocytes during transplantation of
 CC cartilage or chondrocytes; for selection and analysis or for sorting,
 CC isolating or purification of chondrocytes and for in vitro studies of
 CC differentiation of chondrocytes; and as a target for anti-adhesive drugs
 CC or molecules in tendon, ligament, skeletal muscle or other tissues where
 CC adhesion impairs the function of the tissue (all claimed). ISa10 binding
 CC entities can be used to determine the differentiation-state of cells
 CC during embryonic development, angiogenesis or development of cancer, in
 CC pathological conditions such as rheumatoid arthritis, osteoarthritis or
 CC cancer, in tissue regeneration or in therapeutic and physiological
 CC repair of cartilage (claimed). A vaccine comprising the integrin
 CC heterodimer or subunit alpha-10 is also claimed. ISa10 polynucleotides,
 CC vectors, host cells and methods of producing recombinant ISa10 are also
 CC claimed

XX Sequence 22 AA;

Query Match 100.0%; Score 114; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLGFFAHKKIPBEKREKLEQ 22
 |||||
 Db 1 KLGFFAHKKIPBEKREKLEQ 22

RESULT 2

ABP56388
 ID ABP56388 standard; peptide; 19 AA.

XX

AC ABP56388;

XX

DT 11-MAR-2003 (first entry)

XX

DE Polyanionic polymer related peptide #3.

XX

KW Polyanionic polymer; bioactivity; water solubility.

XX

OS Synthetic.

XX

PN WO200277036-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US008614.

XX

PR 21-MAR-2001; 2001US-027705P.

XX

PA (LEUN/) LEUNG D W.

XX

PI Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;

PI Waggoner DW;

XX

DR WPI; 2003-058367/05.

XX

PT Producing monodispersed preparation of polyanionic polymer for therapy,
 PT by expressing vector comprising ligation product of oligonucleotides
 PT encoding glutamate/aspartate residues in host cell and isolating the
 PT product.

XX

PS Example 1; Fig 2; 74pp; English.

XX

CC The present invention describes a method (M) for producing a
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
 CC kD. (M) involves inserting into an expression vector (EV) a ligation
 CC product formed by ligating together oligonucleotides that encode
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
 CC approximately of the same molecular weight. Also described: (1) a
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
 CC another polypeptide at either one end or at both ends of it; (2) a

CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
 CC leukine, where the polyanionic polymer is polyglutamic acid or
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at
 CC least one other nucleotide sequence, where the polyanionic polymer is
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
 CC comprising (III) or a vector that comprises a nucleotide sequence
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
 CC is useful for treating a disease or ailment in an individual by
 CC administering (I) to the individual. (I) is also useful for delivering an
 CC effective amount of a pharmaceutically active agent, a therapeutic
 CC protein or a drug to a patient in need of it, or for diagnostic and
 CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to
 CC ABP56400 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 19 AA;

Query Match 38.6%; Score 44; DB 6; Length 19;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 KIPEEKREKLEQ 22

||:||||:|

Db 2 KMPEEEEEEEEE 15

RESULT 3

AAB59156

ID AAB59156 standard; peptide; 20 AA.

XX

AC AAB59156;

XX

DT 21-MAR-2001 (first entry)

XX

DE Alpha IIB beta 3 binding motif peptide #10.

XX

KW Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
 KW thrombosis; malignancy.

XX

OS Synthetic.

XX

PN WO200073341-A1.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014656.

XX

PR 27-MAY-1999; 99US-00320907.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ginsberg MH, Pfaff M;

XX

DR WPI; 2001-041143/05.

XX

PT Polypeptides useful in construction of structural models for identifying
 PT therapeutic compounds, comprises series of heptad repeats that mimic a
 PT transmembrane domain and cytoplasmic domain attached to the repeats.

XX

PS Disclosure; Page 13; 36pp; English.

XX

CC The present invention relates to a peptide with a series of heptad-
 CC repeats that mimic a transmembrane domain and a selected cytoplasmic
 CC domain attached to the heptad repeats. The invention is useful for
 CC evaluating structure and activity of a selected occupied and clustered
 CC transmembrane protein with the selected cytoplasmic domain and for
 CC identifying therapeutic compounds. It is also useful for identifying a
 CC cytoplasmic domain binding partner. It is also useful for identifying a
 CC interactions with transmembrane proteins such as integrin, which can be
 CC used to treat conditions in which over activity of integrins is involved,


```

XX PF 09-OCT-1997; 97WO-US018331.
XX XX
XX PR 15-OCT-1996; 96US-0028420P.
XX XX
XX PA (UYVA-) UNIV VANDERBILT.
XX PI
XX PI Hawiger JJ, Timmons S, Liu X;
XX XX
XX DR WPI; 1998-251051/22.
XX XX
XX PT Inhibiting cellular adhesion useful e.g. to prevent tumour growth - by
XX PT introducing peptide(s) comprising cell adhesion regulatory domain of an
XX PT adhesion receptor or counter receptor sub-unit expressed by the cell.
XX XX
XX XX Example; Page 23; 76pp; English.
XX CC This is the amino acid sequence of a peptide from human integrin beta-3-
XX CC subunit, which is used in the method of the invention. This method
XX CC involves the inhibition of cellular adhesion, with the use of peptides
XX CC comprising a cell adhesion regulatory domain (CARD) of an adhesion
XX CC receptor or counter receptor subunit expressed by the cell. The method is
XX CC useful in treatments requiring inhibition of cellular adhesion e.g. to
XX CC prevent growth of tumours, since adhesion is required to form tumour
XX CC masses. It can be used to inhibit cellular inflammatory responses,
XX CC (especially when the CARD is an integrin beta or alpha subunit), and to
XX CC treat excessive fibroblast proliferation (especially to heal wounds) when
XX CC the peptide comprises an integrin beta 1 CARD. The method is useful to
XX CC treat coronary and/or vascular diseases, as well as respiratory distress
XX CC syndrome, and retinosis in the blood
XX SQ Sequence 19 AA;

Query Match 36.8%; Score 42; DB 2; Length 19;
Best Local Similarity 47.4%; Pred. No. 65;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 KLGFFAHHKTIPEEKREEK 19
DB 1 KAGFFKXNRPLSEDDDEE 19

RESULT 7
ADA27160
ID ADA27160 standard; peptide; 7 AA.
AC ADA27160;
XX DT
XX DT 20-NOV-2003 (first entry)
XX DE Human integrin 10alpha subunit cytoplasmic domain motif.
XX XX
XX KW cyostatic; antiinflammatory; immunomodulator; neuroprotective;
XX KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
XX KW neurological disorder; blood clotting disorder; food additive;
XX KW preservative; secreted protein; integrin alpha; human.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US2003055231-A1.
XX XX
XX PD 20-MAR-2003.
XX XX
XX PF 29-OCT-2001; 2001US-00984130.
XX XX
XX PR 28-OCT-1998; 98US-0105971P.
XX PR 27-OCT-1999; 99WO-US025031.
XX PR 19-APR-2000; 2000US-0198407P.
XX PR 30-OCT-2000; 2000US-0243792P.
XX PR 18-APR-2001; 2001US-00836353.
XX XX
XX PA (NIJ//) NI J.
XX PA (YOUN//) YOUNG P E.

```

```

PA (KENN//) KENNY J J.
PA (OLSE//) OLSEN H S.
PA (MOOR//) MOORE P A.
PA (WEIY//) WEI Y.
PA (GREE//) GREENE J M.
PA (RUBE//) RUBEN S M.
PA (LIUD//) LIU D.
PA (CROC//) CROCKER P R.
XX XX
XX PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
XX PI Ruben SM, Liu D, Crocker PR;
XX XX
XX DR WPI; 2003-567103/53.
XX XX
XX PT New human secreted nucleic acid molecules and polypeptides, useful for
XX PT preventing, treating, or ameliorating a medical condition, such as
XX PT cancer, inflammation, immune disorders, neurological and blood clotting
XX PT disorders.
XX XX
XX PS Example 53; Page 257; 454pp; English.
XX XX
XX CC The invention relates to an isolated nucleic molecule that is at least
XX CC 9% identical to 18 human cDNA sequences representing 12 novel genes
XX CC encoding secreted proteins or a polynucleotide fragment of the cDNA
XX CC sequence contained in American Type Culture Collection (ATCC) deposit No.
XX CC defined in the specification, its species homologue, a variant or allelic
XX CC variant of the polynucleotide having a polynucleotide capable of
XX CC hybridising under conditions the polynucleotide, where the polynucleotide
XX CC does not hybridise under stringent conditions to a nucleic acid molecule
XX CC having a nucleotide sequence of only A or T residues. Also included are
XX CC recombinant vectors, host cells (for producing the polypeptide), the
XX CC secreted polypeptide (comprising a sequence that is at least 95%
XX CC identical to a polypeptide fragment, domain, epitope, full-length
XX CC protein, variant, allelic variant or species homologue), antibodies that
XX CC specifically bind to the polypeptides, diagnosing, treating, preventing
XX CC or ameliorating a medical condition by administering the polynucleotide
XX CC or the polypeptide, the gene corresponding to the cDNA sequence and
XX CC identifying an activity in a biological assay (by expressing the cDNA
XX CC sequence in a cell, isolating the supernatant, and detecting an activity
XX CC in a biological assay and identifying the protein in the supernatant
XX CC having the activity). The polypeptides, nucleic acids and antibodies are
XX CC useful for diagnosing a pathological condition or a susceptibility to a
XX CC pathological condition, for preventing, treating, or ameliorating a
XX CC medical condition, such as cancer, inflammation and other immune
XX CC disorders, neurological and blood clotting disorders (many examples are
XX CC given in the specification). The nucleic acids are also useful for
XX CC chromosome identification, radiation hybrid mapping or long-range
XX CC restriction mapping. The polypeptides and antibodies are useful for
XX CC providing immunological probes for differential identification of the
XX CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
XX CC agonist or antagonist may also be used as a food additive or preservative
XX CC to increase or decrease storage capabilities, fat content or other
XX CC nutritional components. Novel gene 7 has been identified as encoding
XX CC integrin alpha 11 subunit. The present sequence is the integrin alpha
XX CC subunit conserved cytoplasmic domain motif as found in the gene7 protein
XX CC or its homologue.
XX XX
XX SQ Sequence 7 AA;

Query Match 34.2%; Score 39; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLGFFFAH 7
DB 1 KLGFFFAH 7
| | | | | | |
| | | | | | |

RESULT 8
ADI39445
ID ADI39445 standard; peptide; 7 AA.
XX XX
XX AC ADI39445;

```

XX 22-APR-2004 (first entry)
 XX Integrin alpha10 cytoplasmic domain peptide sequence.
 XX MSC; mesenchymal stem cell; integrin alpha10; integrin alpha11;
 XX cell therapy; tissue repair; cytoplasmic domain.
 XX Unidentified.
 XX WO2003106492-A1.
 XX 24-DEC-2003.
 XX 12-JUN-2003; 2003WO-SE000983.
 XX 14-JUN-2002; 2002SE-00001831.
 XX 14-JUN-2002; 2002US-0388298P.
 XX (CART-) CARTELA AB.
 XX Lundgren-Akerlund E;
 XX WPI; 2004-062518/06.
 XX Marker for mammalian mesenchymal stem cells, useful for identifying and
 PT isolating mesenchymal stem cells, comprising integrin alpha 10 and/or
 PT integrin alpha 11 chain expressed on surface or within the stem cell.
 XX Disclosure; Page 2; 37pp; English.
 XX The invention relates to a marker (I) for mammalian mesenchymal stem
 CC cells (MSC), comprising an integrin alpha10 and/or integrin alpha11 chain
 CC expressed on cell surface of a MSC or intracellular in a MSC. (I) is
 CC useful for identification of a mammalian MSC, for modulating
 CC differentiation of a mammalian MSC and for isolating a mammalian MSC. (I)
 CC is useful for identifying, differentiating and isolating mammalian MSC
 CC from a mixed cell population as useful tools in cell therapy or in repair
 CC of damage tissue. The present sequence represents a sequence from the
 CC integrin alpha10 cytoplasmic domain which is present in the place of a
 CC conserved integrin cytoplasmic domain motif (ADI39444).
 XX Sequence 7 AA;
 Query Match 34.2%; Score 39; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLGFFAH 7
 Db 1 KLGFFAH 7
 RESULT 9
 ABP94377
 ID ABP94377 standard; peptide; 15 AA.
 AC ABP94377;
 XX 28-MAR-2003 (first entry)
 XX HLA protein 121P2A3 peptide #10732.
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002WO-US011359.
 PF 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.

PF 09-APR-2002; 2002WO-US011359.
 XX 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 FI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 263; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX Sequence 15 AA;
 Query Match 34.2%; Score 39; DB 6; Length 15;
 Best Local Similarity 53.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 AHKKIPBEKKREKL 20
 Db 1 ARGKLEBEKKRSEEL 15
 RESULT 10
 ABP93904
 ID ABP93904 standard; peptide; 15 AA.
 XX AC ABP93904;
 XX 28-MAR-2003 (first entry)
 DT HLA protein 121P2A3 peptide #10259.
 DE Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002WO-US011359.
 PF 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.

XX New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.
XX
PS Claim 13; SEQ ID NO 1855; 223pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
CC represent peptides from the 121P2A3 variants of the invention
XX
SQ Sequence 15 AA;

Query Match 34.2%; Score 39; DB 6; Length 15;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AHKKIPEEKREKL 20
| | | | | | | | | |
Db 1 ARGKLEEEKRSEEL 15

RESULT 13
AAU85587
ID AAU85587 standard; peptide; 20 AA.

XX AAU85587;
XX
DT 21-MAY-2002 (first entry)
XX
DE Lung tumour protein L548S peptide #22.
XX
KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic.
XX
OS Homo sapiens.

XX WO200204514-A2.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US022058.

XX 11-JUL-2000; 2000US-00614124.
XX 29-AUG-2000; 2000US-00651563.
XX 08-SEP-2000; 2000US-00658824.
XX 26-SEP-2000; 2000US-00671325.
XX 06-OCT-2000; 2000US-00677419.
XX 30-OCT-2000; 2000US-00702705.
XX 13-DEC-2000; 2000US-00736457.
XX 03-MAY-2001; 2001US-00849626.

XX (CORI-) CORIYA CORP.

XX Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
XX Marxakakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
XX Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX WPI; 2002-164634/21.

XX Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX
PS Claim 2; SEQ ID NO 1855; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumour
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumour protein.
CC This is the amino acid sequence of a lung tumour associated peptide,
CC described in the method of the invention. Note: the sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 34.2%; Score 39; DB 5; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPEEKREE 18
| | | | | | | | | |
Db 8 ARKKVEEEDDEEE 20

RESULT 14
ABU69559
ID ABU69559 standard; peptide; 20 AA.

XX ABU69559;
XX
DT 05-JUN-2003 (first entry)
XX
DE Human lung cancer protein L548S CD4 epitope scanning peptide #22.
XX
KW Human; lung cancer; lung tumour; cytostatic; vaccine; T cell expansion;
XX CD4; CD8; L548S; epitope.
XX
OS Homo sapiens.

XX US2002197669-A1.

XX 26-DEC-2002.

XX 03-MAY-2001; 2001US-00849626.

XX 13-DEC-2000; 2000US-00736457.

XX (BANG/) BANGUR C S.
XX (FANG/) FANGER G R.
XX (WANG/) WANG A.
XX (WANG/) WANG T.
XX (SWIT/) SWITZER A P.
XX (MCNE/) MCNEILL P D.
XX (CLAP/) CLAPPER J D.

XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
XX Clapper JD;

XX WPI; 2003-352750/33.

XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
PT detecting the presence of lung cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating lung cancer.

XX Example 6; Page; 72pp; English.

XX The invention relates to a polynucleotide encoding a lung tumour protein,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:58:57 ; Search time 138 Seconds

(without alignments)
52.927 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFPAHKIPPEEKREKLEQ 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 306921

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	38.6	19	13	US-10-101-487-67
2	44	38.6	20	9	US-09-320-907B-24
3	44	38.6	20	15	US-10-447-292-24
4	43	37.7	20	9	US-09-320-907B-15
5	43	37.7	20	15	US-10-447-292-15
6	42	36.8	16	16	US-10-786-505-26
7	39	34.2	20	9	US-09-736-457-1855
8	39	34.2	20	9	US-09-902-941-1855
9	39	34.2	20	9	US-09-849-626-1855
10	39	34.2	20	14	US-10-017-754-1855
11	39	34.2	20	14	US-10-113-872-1855
12	39	34.2	20	15	US-10-283-017-1855
13	38	33.3	22	9	US-09-864-761-36284

14	37	32.5	20	9	US-09-736-457-1856	Sequence 1856, Ap
15	37	32.5	20	9	US-09-902-941-1856	Sequence 1856, Ap
16	37	32.5	20	9	US-09-849-626-1856	Sequence 1856, Ap
17	37	32.5	20	14	US-10-017-754-1856	Sequence 1856, Ap
18	37	32.5	20	14	US-10-113-872-1856	Sequence 1856, Ap
19	37	32.5	20	15	US-10-283-017-1856	Sequence 1856, Ap
20	36	31.6	13	10	US-09-876-904A-510	Sequence 510, App
21	36	31.6	13	10	US-09-733-179A-5	Sequence 5, Appli
22	36	31.6	14	9	US-09-320-907B-17	Sequence 17, Appl
23	36	31.6	14	10	US-09-733-179A-15	Sequence 15, Appl
24	36	31.6	14	15	US-10-447-292-17	Sequence 17, Appl
25	36	31.6	16	9	US-09-320-907B-16	Sequence 16, Appl
26	36	31.6	16	10	US-09-733-179A-4	Sequence 4, Appli
27	36	31.6	16	15	US-10-447-292-16	Sequence 16, Appl
28	36	31.6	19	15	US-10-350-405-7	Sequence 7, Appli
29	36	31.6	19	15	US-10-324-143-118	Sequence 118, App
30	36	31.6	21	15	US-10-005-305-19	Sequence 19, Appl
31	36	31.6	21	17	US-10-950-010-101	Sequence 101, App
32	36	31.6	22	15	US-10-005-305-20	Sequence 20, Appl
33	36	31.6	22	17	US-10-350-010-100	Sequence 100, App
34	34	29.8	19	14	US-10-059-720-4	Sequence 4, Appli
35	34	29.8	20	9	US-09-880-149-1	Sequence 1, Appli
36	34	29.8	20	13	US-10-038-045-15	Sequence 15, Appl
37	34	29.8	20	14	US-10-177-550-21	Sequence 21, Appl
38	34	29.8	20	14	US-10-345-281-1	Sequence 1, Appli
39	34	29.8	21	14	US-10-057-789-231	Sequence 231, App
40	34	29.8	21	14	US-10-212-628-231	Sequence 231, App
41	34	29.8	21	14	US-10-177-550-5	Sequence 5, Appli
42	34	29.8	21	14	US-10-177-550-26	Sequence 26, Appl
43	34	29.8	21	14	US-09-320-907B-25	Sequence 25, Appl
44	33.5	29.4	15	15	US-10-447-292-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-101-487-67
; Sequence 67, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10101487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-101-487-67

Query Match 38.6%; Score 44; DB 13; Length 19;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 KIPPEEKREKLEQ 22

|||||

DB 2 KMPPEEEEEEE 15

RESUME 10
US-10-017-754-1855
; Sequence 1955, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick

APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C18
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1855
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-754-1855

Query Match 34.2%; Score 39; DB 14; Length 20;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
Db 8 ARKKVEEDEEEE 20

RESULT 11
US-10-113-872-1855
Sequence 1855, Application US/10113872
Publication No. US20030170255A1
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C19
CURRENT APPLICATION NUMBER: US/10/113.872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1855
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-113-872-1855

Query Match 34.2%; Score 39; DB 14; Length 20;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
Db 8 ARKKVEEDEEEE 20

RESULT 12
US-10-283-017-1855
Sequence 1855, Application US/10283017
Publication No. US20030211510A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita

APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C20
CURRENT APPLICATION NUMBER: US/10/283.017
CURRENT FILING DATE: 2002-10-28
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1855
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-283-017-1855

Query Match 34.2%; Score 39; DB 15; Length 20;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
Db 8 ARKKVEEDEEEE 20

RESULT 13
US-09-864-761-36284
Sequence 36284, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864.761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21

```

; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36284
; LENGTH: 22
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007158.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
US-09-864-761-36284

```

```

Query Match      33.3%; Score 38; DB 9; Length 22;
Best Local Similarity 61.5%; Pred. No. 2.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 7 HKKIPPEEKREK 19
   :|||:
Db 3 NKKKEEEEEEEK 15

```

RESULT 14

```

US-09-736-457-1856
; Sequence 1856, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-736-457-1856

```

```

Query Match      32.5%; Score 37; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 8 KKIPEEKREKLEQ 22
   ||: ||: ||:
Db 2 KKVVEEDEEEEEE 16

```

RESULT 15

```

US-09-902-941-1856
; Sequence 1856, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.

```

```

; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-902-941-1856

```

```

Query Match      32.5%; Score 37; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 8 KKIPEEKREKLEQ 22
   ||: ||: ||:
Db 2 KKVVEEDEEEEEE 16

```

```

Search completed: April 6, 2005, 15:11:37
Job time : 138 secs

```

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:50:40 ; Search time 43 Seconds
(without alignments)
38.193 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFFAHKKIPBEKREKLEQ 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 207443

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	37.7	20	1	US-08-214-770-1
2	43	37.7	20	5	PCT-US95-02885-1
3	43	37.7	20	5	PCT-US95-07542-15
4	39	34.2	20	4	US-09-736-457-1855
5	39	34.2	20	6	5225193-7
6	39	34.2	20	6	5225193-7
7	37	32.5	20	4	US-09-736-457-1856
8	36	31.6	20	6	5225193-2
9	36	31.6	20	6	5225193-2
10	36	31.6	21	1	US-08-073-028-25
11	36	31.6	21	1	US-08-127-499A-15
12	36	31.6	21	1	US-08-482-847-15
13	36	31.6	21	3	US-08-554-616-25
14	36	31.6	21	4	US-09-515-965A-1640
15	36	31.6	21	4	US-09-350-841A-1669
16	36	31.6	21	4	US-10-005-305-19
17	36	31.6	22	1	US-08-073-028-24
18	36	31.6	22	3	US-08-554-616-24
19	36	31.6	22	4	US-09-515-965A-1641
20	36	31.6	22	4	US-09-350-841A-1670
21	36	31.6	22	4	US-10-005-305-20
22	35	30.7	21	5	PCT-US95-07542-11
23	34	29.8	13	1	US-08-056-200-11
24	34	29.8	13	1	US-07-987-272A-6
25	34	29.8	13	2	US-08-800-644-11
26	34	29.8	18	2	US-08-649-991-49
27	34	29.8	19	2	US-08-690-011A-4

28	34	29.8	19	3	US-09-299-495F-4	Sequence 4, Appli
29	34	29.8	20	1	US-08-199-776-21	Sequence 21, Appl
30	34	29.8	20	3	US-08-663-731-21	Sequence 21, Appl
31	34	29.8	20	3	US-08-879-338-21	Sequence 21, Appl
32	34	29.8	20	3	US-09-406-781-1	Sequence 1, Appli
33	34	29.8	20	4	US-09-181-941-15	Sequence 15, Appl
34	34	29.8	20	4	US-09-293-238B-21	Sequence 21, Appl
35	34	29.8	20	4	US-09-880-132-1	Sequence 1, Appli
36	34	29.8	20	5	PCT-US95-02044-21	Sequence 21, Appl
37	34	29.8	21	1	US-08-199-776-5	Sequence 5, Appli
38	34	29.8	21	1	US-08-555-579-1	Sequence 1, Appli
39	34	29.8	21	3	US-08-663-731-5	Sequence 5, Appli
40	34	29.8	21	3	US-08-879-338-5	Sequence 5, Appli
41	34	29.8	21	3	US-08-879-338-26	Sequence 26, Appl
42	34	29.8	21	4	US-09-293-238B-5	Sequence 26, Appl
43	34	29.8	21	4	US-09-293-238B-26	Sequence 26, Appl
44	34	29.8	21	5	PCT-US95-02044-5	Sequence 5, Appli
45	33.5	29.4	20	4	US-10-142-935-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-214-770-1
; Sequence 1, Application US/08214770
; Patent No. 523209
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Mark H.
; APPLICANT: O'Toole, Tim
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: INHIBITORS OF INTEGRIN
; TITLE OF INVENTION: ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06410/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-214-770-1

Query Match 37.7%; Score 43; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

```
Qy 1 KLGFFAHKKIPPEEKREE 18
   :|||:|:|:|
Db 1 KVGFFKRNRPPEEDDEE 18

RESULT 2
PCT-US95-02885-1
; Sequence 1, Application PC/TUS9502885
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Mark H.
; APPLICANT: O'Toole, Timothy
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
; TITLE OF INVENTION: OF INTEGRIN ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02885
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,770
; FILING DATE: March 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06410/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US95-02885-1

Query Match 37.7%; Score 43; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KLGFFAHKKIPPEEKREE 18
   :|||:|:|:|
Db 1 KVGFFKRNRPPEEDDEE 18

RESULT 3
PCT-US95-07542-15
; Sequence 15, Application PC/TUS9507542
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
; NUMBER OF SEQUENCES: 20
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07542
```

```
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US95 08/260,514
; FILING DATE: 15-JUN-1994
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens integrin alpha-IIb
PCT-US95-07542-15

Query Match 37.7%; Score 43; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KLGFFAHKKIPPEEKREE 18
   :|||:|:|:|
Db 1 KVGFFKRNRPPEEDDEE 18

RESULT 4
US-09-736-457-1855
; Sequence 1855, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1855
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1855

Query Match 34.2%; Score 39; DB 4; Length 20;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
   :|||:|:|:|
Db 8 ARKKVEEEDDEE 20

RESULT 5
5225193-7
; Patent No. 5225193
; APPLICANT: BARTFAL, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:7
; LENGTH: 20
```



```
5225193-7
Query Match          34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 35.0%; Pred. No. 51;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KLGFFAHKKIPEEKREKL 20
    :||:|||||:|:
Db 1 KSEYLAHRRIPPENIRTRV 20

RESULT 6
5225193-7
; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:7:
; LENGTH: 20
5225193-7

Query Match          34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 35.0%; Pred. No. 51;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KLGFFAHKKIPEEKREKL 20
    :||:|||||:|:
Db 1 KSEYLAHRRIPPENIRTRV 20

RESULT 7
US-09-736-457-1856
; Sequence 1856, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1856

Query Match          32.5%; Score 37; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 95;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KKIPEEKREKLEQ 22
    ||:||||:|:
Db 2 KKVEEDEEQEEEEE 16

RESULT 8
5225193-2
; Patent No. 5225193
; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:7:
; LENGTH: 20
5225193-2

Query Match          31.6%; Score 36; DB 6; Length 20;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 FFAHKKIPEEKR 16
    :||:|||||
Db 3 YLAHRRIPPENIR 15

RESULT 9
5225193-2
; Patent No. 5225193
; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:2:
; LENGTH: 20
5225193-2

Query Match          31.6%; Score 36; DB 6; Length 20;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 FFAHKKIPEEKR 16
    :||:|||||
Db 3 YLAHRRIPPENIR 15

RESULT 10
US-08-073-028-25
; Sequence 25, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; FILE REFERENCE: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-25

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 HKKIPPEEKREKLEQ 22
Db 6 HSLIEESQNOQEKNEQ 21

RESULT 11
US-08-127-499A-15
; Sequence 15, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-15

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 HKKIPPEEKREKLEQ 22
Db 1 HSLIEESQNOQEKNEQ 16

RESULT 12
US-08-482-847-15
; Sequence 15, Application US/08482847

; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-15

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 HKKIPPEEKREKLEQ 22
Db 1 HSLIEESQNOQEKNEQ 16

RESULT 13
US-08-554-616-25
; Sequence 25, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-25

Query Match 31.6%; Score 36; DB 3; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQNQOEKNEQ 21

RESULT 14

US-09-515-965A-1640
Sequence 1640, Application US/09515965A
Patent No. 6823741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sisca, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1640
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1640

Query Match 31.6%; Score 36; DB 4; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQNQOEKNEQ 21

RESULT 15

US-09-350-841A-1669
Sequence 1669, Application US/09350841A
Patent No. 6750008
GENERAL INFORMATION:
APPLICANT: Jéffes, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1669
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: core polypeptide
US-09-350-841A-1669
Query Match 31.6%; Score 36; DB 4; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQNQOEKNEQ 21
Search completed: April 6, 2005, 15:00:24
Job time : 44 secs

This Page Blank (usp10)